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ADS17489
ADR97658
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AAY28901
ADG93406
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ADM38647
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    \begin{array}{c} \mathbf{v} & \mathbf{
    (without alignments)
932.422 Million cell updates/sec
                                                                                                                                                                                                                                                                               September 30, 2005, 13:30:51 ; Search time 20.3248 Seconds
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275
1 QAQQMVQPQSPVAVSQSKPG.....INQQWERTYLGNVLVCTCYG
                                     GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                OM protein - protein search, using sw model
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### ALIGNMENTS

2105692

Total number of hits satisfying chosen parameters:

Title: Perfect score:

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Sequence:

Scoring table:

Searched:

Post-processing: Minimum Match 0% Maximum Match 100%

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Database :

Protein # Fibronect

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base	••	1: A Ge	A_Geneseq_16Dec04: : geneseqp1980s:* : geneseqp1990s:*	16Dec 21980 21990	ec04:* 80s:* 90s:*	X 4 X X	AAY90281; 13-OCT-2000 (first entry)
			geneseqp2001s:*	\$2001 52001	018:*	DE	Human fibronectin protein sequence fragment.
			geneseqp2003as	p2003	03as:*		Streptokinase, SK, hybrid plasminogen activator, fibrin binding region,
		 	geneseqpz0048:* geneseqp20048:*	p2003	0.48:* 0.48:*	KW KW	prasminogen; numan; ildronectin; caromooiytic therapy; cardiovascular disorder; fibronectin.
Pr BC BC	ed. No. ore gre	is the sater the srived	e numbe han or by anal	er of equa lysis	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	SO XX	Homo sapiens. EP1024192-A2.
					SUMMARIES	XX .	02-AUG-2000.
)t	Score	& Query Match	* Query Match Lenath DB	E 0	B 1D Description	XX FIGURE	23-DEC-1999; 99EP-00310541.
							24-DEC-1998; 98IN-DE003825.
C1 C	275	1000		m (N (	Aay90281 Aay28914	XX RA RA RA RA RA	(COUL ) CSIR COUNCIL SCI IND RES.
n 4r	275	100.0			AAKS2//8 human AAU74674 Aau74674 Human	——	Sahni G, Kumar R, Roy C, Rajogopal K, Nihalani D, Sundaram V;
n n	275	100.0	2324	4 C	5 AAE23651 Aae23651 Human pro 1 AAP70373 Human fib	I A	Yadav M;
	275				AAR15468 Human	- A	WPI; 2000-516032/47.
0 0	275				ANGO 1182 ABU07486 Abu07486		N-FOLDS MANS 1034.
10	275	100.0	2328	w w	6 ABR41106 Abr41106 Human fib 6 ABR92078 Human cer	Td .	Hybrid streptokinase-fibrin binding domain polypeptides useful for thrombolytic therapy comprises a streptokinase fused with fibrin binding
127	275				ADB70378 Adb70378 Fibror	FA	domains of human fibronectin.
14.	275				ADE82522 Ade82522	PS	Example 3; Fig 6; 58pp; English.
15	275	100.0	2328	8 7 9 8	8 ADJ37157 Adj37157 Human mal 2 AAW63171 Amino aci	¥8	This sequence represents a human fibronectin fragment, containing fibrin
17	275				AAR60021 Aar60021	88	binding domains. The invention relates to a hybrid plasminogen activator
5 6	275				AAW99595 Human		capable of plasminogen (PG) activation, and fibrin binding regions of
20	272	98.9	_		ADP75952 Adp75952	ខ្ល	human fibronectin, which are from fibrin binding domains (FBD) 4 and 5 or
227	272	98.0	1359	σ <sub>~</sub>	8 ADP75957 Adp75957 Human leu 3 AAR58210 Aart canc	88	l and 2. The hybrid PA possesses the ability to bind with ribrin independently and also characteristically retains a PG activation ability
23	271	98.5		9	Abr58303		which becomes evident only after a pronounced duration, or lag, after
24	271	98.5	642	80 0	Adq39403	ည -	exposure of the PA to a suitable animal or human PG. The hybrid
ς Σ	7/7	98.5	642	ж П	8 ADR67316 Human bla	- ع	Streptokinase-Ilbiin binding domain polypeptides are desta in

Result

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50 QAQQMVQPQSPVAVSQSKPGCYDNGKHYQINQQWERTYLGNVLVCTCYG 98
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Unidentified
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21-JUN-1996
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                                                 RESULT 3
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             hybrids have enhanced fibrin selectivity as well as kinetics of plasminogen activation that are distinct from that of natural streptochiases in being characterised by a temporary delay, or lag of several minutes in the natural rate of the catalytic conversion of plasminogen to plasmin (i.e. delayed-action thrombolysis). The proteins can bind tightly with fibrin in blood clots soon after introduction into blood plasminogen to plasmin, thus significantly activating the circulating blood plasminogen activation process to the site of pathological thrombus. This overcomes systemic plasminogen activation ectivation encountered during clinical use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proteins with cell migration stimulatory activity used in treating wound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention provides a human migration stimulatory factor (MSF) protein. Host cells containing a replicable vector comprising the MSF encoding nucleic acid can be used for the recombinant production of the protein. The polypeptide can be used for modulating cell migration, healing a wound and for preventing scarring. The present sequence represents the human fibronectin
thrombolytic therapy for various kinds of cardiovascular disorders. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Migration stimulatory factor; MSF; cell migration; modulation; human; wound healing; scarring; MSF1-alpha; epitope; fibronectin.
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100.0%; Pred. No. 1.8e-28;
ive 0; Mismatches 0;
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100.0%; Score 275; DB 2;
Best Local Similarity 100.0%; Pred. No. 6e-28;
Matches 49; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY28914 standard; protein; 720 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fibronectin protein sequence
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                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                 of streptokinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 720 AA;
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Gaps

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Indels

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Fibrin-binding peptide, fibronectin, fibrinolysis, fibrinogenesis, thrombus; pulmonary embolus; atherosclerosis; tumour; diagnosis; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                123. .2230
|abel = Fibrin binding domain
note= "11 kDa C-terminal fibrin-binding domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note= "Cys2189-Cys2216 disulfide bond"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note= "Cys2214-Cys2226 disulfide bond"
                                                                                                                                                                                                                                                                                                                                                                                                                                                          note= "Cys2144-Cys2173 disulfide bond"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   171. .2183
note= "Cy82171-Cys2183 disulfide bond"
                                                                                                                                                                                                                                                                                                               39. .467 -
note= "Cys439-Cys467 disulfide bond"
                                                                                                                                                                                                                                                                                                                                        note= "Cys465-Cys477 disulfide bond"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label = 12F1
/note= "type 1 module 12"
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                                                                                                                                                                                                                                                                                                                                                                                                                                           note= "type 1 module 10"
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330, .569
|label = 9F1
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                                                                                                                                   11. .65
/label = 1F1
/note= "type 1 module
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"type 1 module
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/note= "type 1 module
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AAR92778 standard; protein; 2324 AA
                                                                                                                          ocation/Qualifiers
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note= "type 1
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label = 7F1
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|abel = 10F
                                         (first entry)
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label
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                                 (revised)
                                                          Human fibronectin.
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                                                                                                                                                                                        Human fibronectin (AAR92778) has a fibrin-binding site, close to the C-terminus (amino acids 2123-2232 or 2141-2230), covering the 10F1.11F1 module pair of the protein. Fibrin-binding sites can be prepd. by enzymatic cleavage of fibronectin, peptide synthesis or by recombinant DNA techniques. They are used to detect a fibrin-binding target site, to treat disorders involving abnormal fibrinolysis or fibrinogensis, to disrupt blood clots and to aid delivery of medicaments to fibrin- contgines. They show high affinity to and slow dissociation from fibrin, and
                                                                                                                                           New fibrin-binding peptide molecules - used for the diagnosis and treatment of conditions associated with fibrin deposition, e.g. thrombi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Obtaining hematopoietic cell population containing quiescent cells for
                                                                                                                                                                                                                                                                                        Revised record issued on 21-OCT-2004 : Correction to Feature Table Key
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                                                                                                                                                                                                                                                                                                                               Length 2324;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; fibronectin, VLA-4 binding site, very late antigen-4; quiescent haematopoietic cell; HC; apoptosis; CD34+.
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                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                       provide fast diffusion and rapid clearance
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                                                                                                                                                                       Claim 2; Page 104-110; 146pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                      AAU74674 standard; protein; 2324 AA
                                      95WO-US009819
                                                        94US-00283857
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                                                                         (UYNY ) UNIV NEW YORK STATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human fibronectin protein.
                                                                                                                                                                                                                                                                                                                                      Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Williams DA, Bradford
                                                                                             Rostagno AA;
                                                                                                               1996-129333/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-082932/11.
                                                                                                                                                                                                                                                                                                            Sequence 2324 AA;
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                   15-FEB-1996
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The invention relates to obtaining a population of quiescent haematopoietic cells (HG), comprising culturing HC while adhering the cells to a pollypeptide having a very late antigen-4 (VLA-4) binding site, in particular fibronectin polypeptide, so as to expand the number of HC. Where the adhering provides an increased percentage of quiescent HC. Also included are inducing apoptosis of a subpopulation of HC, by contacting the cells with a polypeptide having a VLA-4 binding site under conditions to cause apoptosis of a subpopulation of HC and a medium for culturing HC which enriches quiescent HC, comprising a fibronectin polypeptide. The method is useful for obtaining a cell population containing quiescent haematopoietic cells which are useful for treating a subject. Use of the VLA-4 containing peptide is useful for inducing apoptosis of a subpopulation of CD34+ HC population. The present sequence is human fibronectin which contains then VLA-4 binding site used in the method of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to a method for enhancing proliferation or inducing apoptosis of erythroid progenitor cells (EPCs). The method involves culturing haematopoietic cellular populations containing EPCs in the presence of a polypeptide having an integrin very late antigen (VLA)-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human, proliferation, apoptosis, erythroid progenitor cell; EPC, VLA, integrin very late antigen, haematopoietic cell; induced disorder; genetic disorder; congenital erythroid disorder; polycythaemia; anaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
use in treating a subject, by expanding the cells while adhered polypeptide containing binding sites for integrins on the cells.
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100.0%; Pred. No. 2.4e-27;
ive 0; Mismatches 0;
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                                                                                                                        Disclosure; Page 51-61; 63pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 55-64; 66pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAE23651 standard; protein; 2324 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cooper R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-MAY-2000; 2000WO-US012961.
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nes 49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kapur R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-121963/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2324 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200187037-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Williams DA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-NOV-2001
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(revised)
(first entry)

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Fibrin-imaging; atherosclerosis; thrombus inhibitor.
                                        AAR15468 standard; protein; 2327 AA
                                                                                                                            Human fibronectin.
                                                                                                                                                                                                                                                       21-MAY-1990;
                                                                                       25-MAR-2003
12-MAR-1992
                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                       WO9117765-A.
                                                                                                                                                                                                                              28-NOV-1991
                                                                 AAR15468;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 8
                RESULT 7
                             AAR15468
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5 or VLA-4 binding site. The EPCs are useful for treating patients having induced, genetic or congenital erythroid disorders. Methods of the invention are useful in diagnostic assays of progenitor cells, e.g. cells occurring in pathologic states such as anaemia or polycythaemia and in the study of erythroid cell development. They are used in the screening of agents which inhibit or prevent apoptosis of erythroid cells. The present sequence is a human protein related to the modulation of prolliferation of EPCs. This sequence is used in the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The product may be expressed from a transformed micro-organism, esp. E.coli. FN binds to fibrin, heparin and Staphylococcus aureus, and may be used to target a therapuetic agent onto natural fibrin eg. a blood clot. It may also be used in affinity purification of a polypeptide, conjugated to the collagen binding site of FN and immobilised on a collagen surface. (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New fibronectin polypeptide sequence with affinity for collagen etc. - useful for targetting therapeutic substances on natural fibrin, for use in affinity purificn. of polypeptide(s) etc.
                                                                                                                                                                  Gaps
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                                                                                                                                        Length 2324;
                                                                                                                                                                                          1 QAQOMVQPQSPVAVSQSKPGCYDNGKHYQINQQWERTYLGNVLVCTCYG 49
                                                                                                                                                                                                     OAQQMVQPQSPVAVSQSKPGCYDNGKHYQINQQWERTYLGNVLVCTCYG 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 275; DB 1; Length 2327; 100.0%; Pred. No. 2.4e-27; tive 0; Mismatches 0; Indels 0
                                                                                                                                                                 0; Indels
                                                                                                                                       100.0%; Score 275; DB 5;
100.0%; Pred. No. 2.4e-27;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                              AAP70373 standard; protein; 2327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 11; Fig 3A; 32pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BIOTECHNOLOGY LTD
                                                                                                                                                                                                                                                                                                                                                                   Human fibronectin gene product.
                                                                                                                                                                                                                                                                                                                                                                                             FN; collagen; fibrin; heparin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      85GB-00016421.
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                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                 49; Conservative
                                                                                                                                                                                                                                                                                                                                 (revised)
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                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2327 AA;
                                                                                                               Sequence 2324 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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                                                                                                                                                                                                                                                                                                                              25-MAR-2003
11-MAR-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-JAN-1987
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Baralle FE;
                                                                                                                                                                                                                                                                                                       AAP70373;
                                                                                                                                        Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    derive polypeptides which are identical to part of the fibrin- binding domain (FBD) of fibronectin. These polypeptides can be used to inhibit thrombus formation, or (coupled to a thrombolytic agent) to induce thrombolytis agent, est to treat wounds, e.g. in skin, eyes or tendons (in conjunction with a polypeptide which includes a part of the cell-binding domain (CBD) of fibronectin). These polypeptides are easier to prepare than the full 31kD polypeptide. It can also be used to image fibrincontg. materials, esp. a thrombus or athero- sclerotic plaque, pref. using a gamma counter. (Updated on 25-MAR-2003 to correct PI field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The amino acid sequence is that of human fibronectin, this can be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                              New fibrin binding domain polypeptide(s) - useful in imaging fibr:
contg. substances, to inhibit thrombus formation and treat wounds
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                                                                                                                                                                 Panet A, Hartman J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 QAQQMVQPQSPVAVSQSKPGCYDNGKHYQINQQWERTYLGNVLVCTCYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 QAQQMVQPQSPVAVSQSKPGCYDNGKHYQINQQWERTYLGNVLVCTCYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 275; DB 2; 100.0%; Pred. No. 2.4e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                 Guy R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAG68182 standard; protein; 2328 AA
                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Fig 2; 191pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fibronectin protein SEQ ID NO:98.
                                                                                                                                                                 Werber M,
90US-00526397.
                                                     90US-00526397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-JAN-2002 (first entry)
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Matches 49; Conservative
                                                                                                           (BIOT-) BIO-TECHN GEN
                                                                                                                                                                 Levanon A,
                                                                                                                                                                                                                                                 WPI: 1991-369004/50.
                                                                                                                                                                                                                                                                                                                                                             contg. substances,
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                                                     21-MAY-1990;
                                                                                                                                                                                           Shaked H;
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Gaps

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52

1 QAQQMVQPQSPVAVSQSKPGCYDNGKHYQINQQWERTYLGNVLVCTCYG 49

49; Conservative

Local Similarity

Best Loc Matches

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QAQQMVQPQSPVAVSQSKPGCYDNGKHYQINQQWERTYLGNVLVCTCYG

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The invention describes genes (1) which are differentially regulated in prostate cancer. (2) Is useful for diagnosing a prostate cancer in a semple comprising prostate tissue, which involves determining the number of target genes which are differentially-regulated in the sample, where to target genes which are differentially-regulated in the sample, where to prostate cancer. (3) Is useful for assessing a therapeutic or preventive intervention in a subject having a prostate cancer, which involves contention in a subject having a prostate cancer. Which involves contenting the expression levels in a sample comprising prostate cancer. Preferably, the expression levels of at least 10 genes are determined. (1) is also useful for identifying agents that modulate a biological activity of a polypeptide differentially-regulated in prostate cancer. (2) is also useful for identifying agents that modulate a biological activity of the polypeptide, and cativity of a polypeptide differentially-regulated in postate cancer. (2) is useful as molecular markers, as qual targets, and for detecting, the test agent to modulate a biological activity of the polypeptide, and determining whether the test agent modulates the biological activity. (1) is useful as molecular markers, as qual targets, and for detecting, products are used in the diagnostic test to assay for presence of concerned products are used in the diagnostic test to assay for presence of cancer (2), in tissue sections, in biopsy sample, in total NN, in lymph, in blood etc. (1) is useful for assessing cancer e.g., to determine the type of cancer, its stage of development, the nature of genetic defect, etc. (2) the polypeptide and thus activity of products are used in the diagnostic test to assay for presence of cancer (3), in therapeutic applications to reat pornate cancer. The identification of specific genes, and groups of genes, expressed in pathways which are useful in diagnostic, therapeutic, and clinical in therapeutic applications of genes are not prostate cancer. T
                                             Novel genes which are differentially regulated in prostate cancer, useful for diagnosing prostate cancer in prostate tissue sample and assessing therapeutic or preventive intervention in prostate cancer patients.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; high bone mass; HBM; LRP5; LRP6; transgenic; bone mass modulation; gene therapy; bone density modulation; bone strength; trabecular number; bone size; bone tissue connectivity; bone disease; osteoporosis; osteomalacia; rickets; Paget's disease; neoplasm of the bone.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 QAQQMVQPQSPVAVSQSKPGCYDNGKHYQINQQWERTYLGNVLVCTCYG
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100.0%; Pred. No. 2.4e-27;
ive 0; Mismatches 0;
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                                                                                                                                             Claim 1; Page 378-386; 416pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABR41106 standard; protein; 2328 AA.
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Matches 49; Conservative
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N-PSDB; ABX10391.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABR41106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes the human Zmax1 gene and the high bone mass (HBM) gene, which are found on chromosome 11q13.3. The Zmax1 and HBM genes have osteopathic activities. The genes and be used in gene therapy, antisense therapy and in the production of vaccines. They can be used in the diagnosis and treatment of bone disorders including osteoporosis, the diagnosis and treatment of bone disorders including osteoporosis, ABAB2038 to ABAB2700 and AAG68193 to AAG68193 represent sequences used in the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Prostate cancer; gene expression; differential regulation; molecular marker; drug target; cancer detection; cancer diagnosis; cancer staging; cancer grading; cancer assessing; cancer monitoring
                                                                                                                                                                                                                                                                                                                                                                                                                                                          proteins useful for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      / Match 100.0%; Score 275; DB 4; Length 2328; Local Similarity 100.0%; Pred. No. 2.4e-27; Los 49; Conservative 0; Mismatches 0; Indels 0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       New high bone mass (HBM) and Zmax1 genes and proteins useful modulating bone mass for the treatment of e.g. osteoporosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 QAQQMVQPQSPVAVSQSKPGCYDNGKHYQINQQWERTYLGNVLVCTCYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein differentially regulated in prostate cancer #89.
                                                                                                                                                                                                                                                                                                                                                      Johnson ML;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 76; Page 408-413; 443pp; English.
                                                                                                                                                                                                                                                                                                                                                      Recker RR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABU07486 standard; protein; 2328 AA.
                                                                                                                                                                                                                                                                                                 (GENO-) GENOME THERAPEUTICS CORP.
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                                                                                                                                                                      21-JUN-2000; 2000WO-US016951.
                                                                                                                                                                                                                   05-APR-2000; 2000US-00543771
05-APR-2000; 2000US-00544398
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                                                                                                                                                                                                                                                                                                                                                      Little RD,
                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-657171/75.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2328 AA;
                                                                WO200177327-A1
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                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-0CT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-JAN-2003
                                                                                                                   18-OCT-2001
                                                                                                                                                                                                                                                                                                                                                    Carulli JP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABU07486;
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order in ABR22047 to ABR22164. A higher level of expression of (1) than normal indicates the presence of cervical cancer. Also described: (1) a vector (II) containing (I); (2) a host cell (III) containing (I); and (3) assessing (MI) whether a patient is afflicted with cervical cancer, comprising comparing the level of expression of a marker in a control nor cervical cancer sample, where a significant increase in the level of expression of the marker in the patient's sample relative to that in the control sample is an indication that the patient is afflicted with cervical cancer. (I) has cytostatic activity, and can be used in gene therapy and in vaccines. (I) is useful in detecting, characterising, preventing and treating human cervical cancers. (I) may also be used in monitoring clinical trials
                                                                                                                                                                                                                                                                                                                                                New isolated nucleic acid molecule useful for detecting, characterizing,
                                                                                                                                                                                                                                                                                                                                                                                         preventing and treating human cervical cancers, in various prognostic and diagnostic assays, in pharmacogenomics and in monitoring clinical trials
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACF12828 to ACF12947 encode the human cervical cancer marker proteins (I)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cancer; malignant pleural mesothelioma; MPM; lung adenocarcinoma; squamous carcinoma; medulloblastoma; prostate cancer; breast cancer; diffuse large B-cell lymphoma; follicular lymphoma; ovarian cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 QAQQMVQPQSPVAVSQSKPGCYDNGKHYQINQQWERTYLGNVLVCTCYG 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 QAQQMVQPQSPVAVSQSKPGCYDNGKHYQINQQWERTYLGNVLVCTCYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 275; DB 6; 100.0%; Pred. No. 2.4e-27;
                                                                                                                                                                                                                       Schlegel R, Chen Y, Zhao X, Monahan JE,
Gannavarapu M, Glatt K, Hoersch S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 4; Page 212-217; 386pp; English.
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                                                                                             13-JUN-2001; 2001US-0298159P.
14-NOV-2001; 2001US-0335936P.
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                         12-JUN-2002; 2002WO-US018638
                                                                         13-JUN-2001; 2001US-0298155P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-SEP-2002; 2002WO-US028203
                                                                                                                                                                       (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-DEC-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fibronectin SEQ ID NO:70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               49; Conservative
                                                                                                                                                                                                                                                                                                WPI; 2003-156967/15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2328 AA;
                                                                                                                                                                                                                                                                                                                          N-PSDB; ACF12859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO2003021229-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         human.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to novel transgenic animals expressing the high bone mass (HBM) gene, expressing the corresponding wild type HBM gene, comprising an alteration of the gene encoding LRPS or LRP6, or expressing an LRP5 that is modulated by an altered gene control sequence introduced by homologous or non-homologous recombination. The transgenic animals are for the study of bone density modulation or bone mass modulation. The invention may have a use in gene therapy. The transgenic animals and nucleic acids are for the study of bone density modulation, where the conceives in more than one parameter selected from bone density, bone aspecies in more than one parameter selected from bone density, bone strength, trabecular number, bone size, or bone tissue connectivity. The transgenic animals, nucleic acids and methods are useful for identifying molecules involved in bone development, and for developing pharmaceutical compositions, which may be employed for treating or preventing bone diseases, e.g. osteoporosis, osteomalacia, rickets, Paget's disease, or neoplasms of the bone. The transgenic animals and nucleic acids are also useful in methods for diagnosing diseases involved in bone development, or characterised by reduced bone density or mass. The present sequence is used in the exemplification of the invention
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                                                                                                                                                                                                                                                                                                                                                                                            New transgenic animals (e.g. mice), useful as models for studying bone density modulation, developing drugs for treating or preventing bone diseases (e.g. osteoporosis), or diagnosing diseases characterized by reduced bone density.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 QAQQMVQPQSPVAVSQSKPGCYDNGKHYQINQQWERTYLGNVLVCTCYG 49
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                                                                                                                                                                                                                                                                                                Bodine PV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure, Page 532-538; 603pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABR92078 standard; protein; 2328 AA
                                                                                                                                                                                                                    (GENO-) GENOME THERAPEUTICS CORP
                                                                                                                                                                                                                                                                                              Bex FJ, Yaworsky PJ,
                                                                                                                       17-MAY-2001; 2001US-0291311P.
01-FEB-2002; 2002US-0353058P.
                                                                                             11-MAY-2001; 2001US-0290071P.
                                             13-MAY-2002; 2002WO-US014876.
                                                                                                                                                                       04-MAR-2002; 2002US-0361293P.
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                                                                                                                                                                                                                                                                                                                                              WPI; 2003-129278/12
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                                                                                                                                                                                                                                              (AMHP ) WYETH.
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                                                                                                                                                01-FEB-2002;
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21-NOV-2002
                                                                                                                                                                                                                                                                                              Babij P,
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Length 2328;

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2003-129214/12.
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                        P-PSDB; ADB98703
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                                                                                                                                                                                                                                                                                                                                                                       RESULT 14
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                                                                                                                                                                The present invention describes a method (MI) for diagnosing the presence of cancer cells or non-cancer cells in a tissue sample, or determining the prognosis or outcome of a cancer patient. Mi involves providing a set of genes that are differentially expressed in cancerous or non-cancerous conditions, determining the expression levels of the set of genes and calculating a ratio of the expression levels of the differentially capression levels of the differentially or non-cancer cells in a tissue sample, where the cancer is malignant pleural mesothelioma (MPW), lung adenocarcinoma, squamous carcinoma, prostate cancer, breast cancer, difficuse large B-cell lymphoma, follicular lymphoma and ovarian cancer, difficuse large B-cell lymphoma, follicular lymphoma and ovarian cancer, difficuse large B-cell lymphoma, follicular lymphoma and ovarian cancer, difficator determining prognosis or outcome of a cancer patient. The ratio of expression levels cancer class, and/or cancer prognosis, and indicator of cancer type, cancer class, and/or cancer prognosis. The present sequence represents a human protein which is used in an example from the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                            Diagnosing cancer cells in tissue sample, or determining prognosis or outcome of cancer patient, by calculating ratio of expression levels of genes that are differentially expressed in cancer and non cancer tissues.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 275; DB 7; Length 2328; 100.0%; Pred. No. 2.4e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Morales A, Yaworsky PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QAQQMVQPQSPVAVSQSKPGCYDNGKHYQINQQWERTYLGNVLVCTCYG
                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                   Gullans SR, Bueno R;
                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                              Claim 77; Page 369-376; 396pp; English.
           (BGHM ) BRIGHAM & WOMENS HOSPITAL INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADB98726 standard; protein; 2328 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Anisowicz A, Graham JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         bone mass modulation; osteoporosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GENO-) GENOME THERAPEUTICS CORP
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17-MAY-2001; 2001US-029111P.
01-FEB-2002; 2002US-0351058P.
04-MAR-2002; 2002US-0351293P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-MAY-2002; 2002WO-US014877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 100.
es 49; Conservative
                                   Jensen RV,
                                                           WPI; 2003-290233/28.
                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2328 AA;
                                                                       N-PSDB; ADB70377
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-NOV-2002
                                   Gordon GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADB98726;
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                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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The present invention relates to High Bone Mass (HBM), LRPS (Zmax1) and LRP6 mutants, which results in a HBM-like phenotype when expressed in a cell. The HBM-like phenotype results in bone mass modulation and/or lipid level modulation. The invention is useful for diagnosing a HBM-like phenotype in a subject and for preparing a composition for modulating bone mass and/or lipid levels in a subject suffering from e.g. osteoporosis. The present sequence was used to illustrate the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ne present invention relates to regulating LRP5, LRP6 or HBM activity in subject comprising administering a composition which modulates a Dkk
New nucleic acid comprising a mutation in LRP5 or LRP6, useful for diagnosing a HBM-like phenotype in a subject and for preparing a composition for modulating bone mass and/or lipid levels in a subject
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LRP5; LRP6; HBM; Dkk activity; Osteopathic; Antiinflammatory; Antiarthritic; bone mass disorders; osteoporosis; hypercalcaemia; hyperostosis; osteogenesis; Wnt signaling.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human protein sequence related to the invention #12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 275; DB 7;
100.0%; Pred. No. 2.4e-27;
iive 0; Mismatches 0;
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                                                                                                                                                                     Disclosure; SEQ ID NO 677; 629pp; English.
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                                                                                                     suffering from e.g. osteoporosis.
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01-FEB-2002; 2002US-0353058P.
04-MAR-2002; 2002US-0361293P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-MAY-2002; 2002WO-US015982.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match
Best Local Similarity 100...
Local 49; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human, malignant pleural mesothelioma, MPM; tumour; lung adenocarcinoma; squamous carcinoma; medulloblastoma; prostate cancer; breast cancer; diffuse large B-cell lymphoma; follicular lymphoma; ovarian cancer;
activity. The method is useful for modulating lipid levels and/or bone mass, and is useful in treating or diagnosing abnormal lipid levels and bone mass disorders, such as osteoporosis, bond fracture, age-related loss of bone, a chondrodystrophy, drug-induced bone disorder, high bone turnover, hypercalcaemia, hypercostosis, osteogenesis, imperfecta, osteomalacia, osteomyelitis, Paget's disease, osteoarthritis, and rickets. Modulators of Dkk activity are useful for as reagents in studying bone mass and lipid level modulation, in modulating Wht signaling, or treating Dkk-mediated disorders. The present sequence represents a human protein sequence related to the invention.
                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                          1 QAQQMVQPQSPVAVSQSKPGCYDNGKHYQINQQWERTYLGNVLVCTCYG 49
                                                                                                                                                                                     Length 2328;
                                                                                                                                                                                                                                                          QAQQMVQPQSPVAVSQSKPGCYDNGKHYQINQQWERTYLGNVLVCTCYG
                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                           Human malignant pleural mesothelioma (MPM) protein #31.
                                                                                                                                                                                                                 ..
                                                                                                                                                                                  100.0%; Score 275; DB 7;
100.0%; Pred. No. 2.4e-27;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                          ADJ37157 standard; protein; 2328 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-SEP-2001; 2001US-0317389P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-SEP-2002; 2002US-00236031
                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                 Query Match
Best Local Similarity 100.'
Matches 49; Conservative
                                                                                                                                                          Sequence 2328 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cytostatic
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The invention relates to a method of diagnosing the presence of cancer cells or non-cancer cells in a tissue sample, determining prognosis or outcome of a cancer patient, selecting a course of treatment for a subject having or suspected of having malignant pleural mesothelioma (MPM) and evaluating treatment of MPM comprising determining the ratio of the expression level of a set of genes differentially expressed in a cancer tissue. The cancer is chosen from MPM, lung adenocarcinoma, squamous carcinoma, medulloblastoma, prostate cancer, breast cancer, diffuse large B-cell lymphoma, follicular lymphoma and ovarian cancer. The method is useful for diagnosing MPM in a subject suspected of having MPM which involves obtaining a tissue sample suspected of being cancerous

Diagnosing the presence of cancer or non-cancer cells in tissue sample, useful for diagnosing malignant pleural mesothelioma comprises determining ratio of expression level of a set of genes expressed in

Claim 77; SEQ ID NO 70; 53pp; English.

cancer tissues

Gullans SR, Bueno R;

Gordon GJ, Jensen RV, WPI; 2004-141744/14.

N-PSDB, ADJ37156.

(BGHM ) BRIGHAM & WOMENS HOSPITAL INC

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from a subject and determining the expression of nucleic acid markers or its expression products in the tissue sample. This sequence represents a human MPW protein of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html.
                                                                                                                                                                                                                              Gaps
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0
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                                                                                                                                                                                                                                                                                                                  53
                                                                                                                                                                                 Length 2328;
                                                                                                                                                                                                                                                                        1 QAQQMVQPQSPVAVSQSKPGCYDNGKHYQINQQWERTYLGNVLVCTCYG
                                                                                                                                                                                                                                                                                                             5 QAQQMVQPQSPVAVSQSKPGCYDNGKHYQINQQWERTYLGNVLVCTCYG
                                                                                                                                                                               100.0%; Score 275; DB 8;
100.0%; Pred. No. 2.4e-27;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                              49; Conservative
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                                                                                                                                       Sequence 2328 AA;
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

September 30, 2005, 13:30:51; Search time 7.5627 Seconds (without alignments) 623.404 Million cell updates/sec

US-09-492-971B-15\_COPY\_4\_52

275 1 QAQQMVQPQSPVAVSQSKPG.....INQQWERTYLGNVLVCTCYG 49 Perfect score: Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database

PIR 79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### CITAMADITE

	Description	fibronectin precur	fibronectin precur		fibronectin - Afri	fibronectin - mous	fibronectin - chic	fibronectin - east	chordin precursor	5-aminolevulinate	5-aminolevulinate	hypothetical prote	polyamine transpor	hypothetical prote	inositol 1,3,4-tri	hypothetical prote	beta-microseminopr	copia polygrotein	plasmin (EC 3.4.21	hypothetical prote	protein-tyrosine k		amine oxidase (cop	copia polyprotein	thrombospondin 1 p	copia polyprotein	hypothetical prote	adenosylmethionine	hypothetical prote	isoleucine-tRNA li
SUMMARIES	ID	FNHU	S14428	FNBO	A43908	A49173	A29355	151279	A55195	SYMSAL	SYHUAE	S03412	C97433	AD2651	T10544	T29818	A34567	F60767	A40522	T45056	S24551	T22754	A48646	PC1232	TSHUP1	OFFFCP	C82800	B84964	AD2565	F71823
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d	Query Match	100.0	93.5	92.7	70.5		28.9				20.7	20.5	20.5	20.5	20.0	20.0	19.8	19.8	19.8	19.8	19.8	19.8	19.8	19.8	19.8	19.8	19.6	19.6	19.6	19.6
	Score	275	257	255	194	110	79.5	67.5	57.5	57	57	56.5	56.5	56.5	52	22	54.5	54.5	54.5	54.5	54.5	54.5	54.5	54.5	4.	4	54	54	54	24
	Result No.	1	2	m	4	S	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

hypothetical prote	hypothetical prote	UDP-3-0-[3-hydroxy	UDP-3-0-[3-hydroxy	gamma-glutamyltran	gamma-glutamyltran	plastoquinol-plast	leukocyte antigen	pollen-specific pr	thrombospondin 1 p	hypothetical prote	hypothetical prote	Distal-less (D11)	hypothetical prote	conserved hypothet	polyhydroxyalkanoi
T46228	T24599	S47342	D64102	F64659	H71856	S75804	A39574	S22495	A40558	E82622	E75613	A42103	AD2532	E90304	139685
7	N	~	~	~	~	N	Н	0	0	~	~	N	0	~	0
662	321	339	341	267	567	133	219	554	1170	172	214	250	472	520	590
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2	23	23	23	53	23	52.5	52.5	52.5	52.5	52	52	52	25	25	25
23															

## ALIGNMENTS

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fibronectin precursor [validated] - human
NiAlternate names: fibronectin splice form ED-A
C;Species Homo sapiens (man)
C;Species Homo sapiens (man)
C;Species Homo sapiens (man)
C;Species Homo sapiens (man)
C;Date: 27-Nov-1985 #sequence revision 31-Mar-1993 #text change 09-Jul-2004
C;Accession: A56460; A26264; S03917; A24854; A24476; A91008; A93529; A21011; A90495; A2
R;Dean, D.C.; Bowlus, C.L.; Bourgeois, S.
R;Dean, D.C.; Bowlus, C.L.; Bourgeois, S.
R;Acference number: A26460; MUID:87175578; PMID:3031656
A;Accession: A26460
A;Molecule type: DNA
A;Residues: 1-49 cDEA>
A;Cross-references: UNIPROT:P02751; UNIPROT:Q14327; GB:MIS801; NID:g182686; PIDN:AAA533
C;Date: A; Ruoslahti, B.
B;Oldberg, A.; Ruoslahti,
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A; Accession: A26284

A; Residues: 1447-1540 < OLD>
A; Roces: the authors translated the codon TrC for residue 1494 as Glu
R; Paolella, G.; Henchcliffe, C.; Sebastio, G.; Baralle, F.E.
Nucleic Acida Ree. 16, 3345-3557, 1988
A; Title: Sequence analysis and in vivo expression show that alternative splicing of ED-A; Reference number: \$00848; MUID:88233940; PMID:3375063
A; Recension: \$03317
A; Molecule type: DNA
A; Residues: 1594-1767, 'V', 1769-1783 < PAO>
A; Residues: 1594-1767, 'V', 1769-1783 < PAO>
A; Residues: Lanslated the codon AC for residue 1631 as Asp
R; Vibe-Pedersen, K.; Magnusson, S.; Baralle, F.E.
FEBS Lett. 207, 287-291, 1986
A; Title: Donor and acceptor splice signals within an exon of the human fibronectin gene A; Reference number: A24854; MUID:87030929; PMID:3770201

A; Molecule type: DNA A; Residues: 1992-2147 < VIB> A; Residues: 1992-2147 < VIB> A; Cross-references: GB:X04530; NID:g31436 A; Cross-references: GB:X04530; NID:g31436 B; Guman, A.; Yamada, K.M.; Kornblihtt, A. FEBS Lett. 207, 145-148, 1986 A; Title: Human fibronectin is synthesized as a pre-propolypeptide. A; Reference number: A24476; MUID:87030890; PMID:3770189 A; Recession: A24476 A; Residues: 10-14, 'O', 16-38 < GUT> A; Residues: 11-14, 'O', 16-38 < GUT> B; Kornblihtt, A.R.; Unecawa, K.; Vibe-Pedersen, K.; Baralle, F.E. BMBO J. 4, 1755-1759, 1985 A; Title: Primary structure of human fibronectin: differential splicing may generate at

14:33:33

Sep 30

Fr.

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A;Molecule type: protein
A;Residues: 293-301 <GRI>
Kclalaycay, J.; Pande, H.; Lee, T.; Borsi, L.; Siri, A.; Shively, J.E.; Zardi, L.
J. Biol. Chem. 260, 12136-12141, 1985
A;Title: Primary structure of a DNA- and heparin-binding domain (domain III) in human pl.
A;Reference number: A23901; MUID:86008277; PMID:3900070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Molecule type: protein
A,Residues: 616-677, Q', 679-703, 'PT', <CAL>
A,Residues: 616-677, Q', 1679-703, 'PT', <CAL>
A,Residues: 616-677, Q', 1679-703, 'PT', Sundelin, J.; Lind, P.; Peterson, P.A.
J. Biol. Chem. 257, 9593-9597, 1982
A,Title: The cell attachment domain of fibronectin. Determination of the primary structu.
A,Reference number: A92386; MUID:82265604; PMID:7050098
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A;Residues: 1589-1630, T',1722-2058 <GAR3>
A;Residues: 1589-1630, T', 1722-2058 <GAR3>
R;Tressel, T.; McCarthy, J.B.; Calaycay, J.; Lee, T.D.; Legesse, K.; Shively, J.E.; Pand' Biochem. J. 274, 731-738, 1991
A;Title: Human plasma fibronectin. Demonstration of structural differences between the A A;Reference number: S14357; MUID:91190085; PMID:2012601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A,Molecule type: protein
A,Residues: 2071-2080,2112-2356 <GAR4>
C,Comment: The extra domain and connecting strand 3 are subject to developmental and tis
C,Comment: The cellular and plasma fibronectins are high molecular weight glycoproteins.
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A;Map position: 2q34-2q34
A;natons: 49/3, 1266/1, 1357/1; 1487/1; 1541/1; 1631/1; 1721/1; 1991/1; 2145/1
A;natons: 49/3, 1266/1, 1357/1; 147/1; 1487/1; 1541/1; 1631/1; 1721/1; 1991/1; 2145/1
C;Superfamily: fibronectin; fibronectin type I repeat homology; fibronectin type II repe
C;Keywords: acute phase; alternative splicing; cell adhesion; collagen binding; duplicating; 27.231/Domain: signal sequence #status predicted (SIG)
F;27-31/Domain: propeptide #status predicted (SIG)
F;32-2386/Product: fibronectin #status experimental <MAT>
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R;Griffin, C.A.; Calaycay, J.; Shively, J.E.; Smith, R.L.
Thromb. Res. 43, 469-477, 1986
A;Title: Two plasma fibronectin fragments with different gelatin-binding properties.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Characterization of a 38
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A,Molecule type: protein
A,Residues: 1441-1548 «PIE»
A,Note: residues 1524-1527 are responsible for the cell-binding activity
R,Garcia-Pardo, A.; Rostagno, A.; Frangione, B.
Biochem. J. 241, 923-928, 1987
A;Title: Primary structure of human plasma fibronectin. Characterization
A,Reference number: A32517; MUID:87241275; PMID:3593230
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Figure 608/Domain: fibronectin type I repeat homology c1F6>
Figure 6040/Domain: fibronectin type II repeat homology c2F1>
Figure 61/Domain: fibronectin type II repeat homology c2F2>
Figure 608/Domain: fibronectin type II repeat homology c2F2>
Figure 608/Domain: fibronectin type I repeat homology c1F7>
Figure 608/Domain: fibronectin type I repeat homology c1F7>
Figure 608/Domain: fibronectin type II repeat homology c1F9>
Figure 608/Domain: fibronectin type III repeat homology c1F9>
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F;719-801/Domain: fibronectin type III repeat homology <3FB>
F;810-891/Domain: fibronectin type III repeat homology <3FC>
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F;52-272/Domain: fibrin and heparin binding <FHB>
F;52-87/Domain: fibronectin type I repeat homology <LFI>
F;97-135/Domain: fibronectin type I repeat homology <LFI>
F;141-179/Domain: fibronectin type I repeat homology <LF3>
F;186-225/Domain: fibronectin type I repeat homology <LF3>
F;231-270/Domain: fibronectin type I repeat homology <LF4>
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A; Residues: 1614-1650, T', 1722-2081, 2113-2244 <TRE>
R; Residues: 1614-1650, T', 1722-2081, 2113-2244 <TRE>
R; Garcia-Pardo, A.; Pearlstein, E.; Frangione, B.
Biol. Chem. 260, 10326-10325, 1985
A; Title: Primary structure of human plasma fibronectin.
A; Reference number: A23891; MOID:85261459; PMID:4019516
                                                                                                                                                                                           A; Reference number: A60904; MUID:87019725; PMID:3532418
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A; Molecule type: mRNA
A; Residues: 1948-2067 < UME>
A; Cross-references: GB:MZ7589; NID:G182705; PIDN:AAA52465.1; PID:G182706
A; Cross-references: GB:MZ7589; NID:G182705; PIDN:AAA52465.1; PID:G182706
A; Accession: B22245
A; Molecule type: mRNA
A; Residues: 1975-1991; 2017-2039 < UM2>
A; Cross-references: GB:MZ7590
A; Title: Human liver fibronectin complementary DNAs: identification of two different mes A; Reference number: 152394; MUID:87026578; PMID:3021206
A; Accession: 165273
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1976-1990, 2016-2018 'N', 2020-2081, 2113-2127 < SEK>
A; Cross-references: GB:M14060; NID:G182701; PIDN:AAA52464.1; PID:G182704
A; Cross-references: GB:M14060; NID:G182701; PIDN:AAA52464.1; PID:G182704
A; Cross-references: GB:M14060; NID:G183222, 1983
A; Title: Isolation and characterization of CDNA clones for human and bovine fibronectine
A; Accession: A; A; Cross-reference number: A21165; MUID: 83221567; PMID: 6304699
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A; Residues: 1434-1537 <-012>
A; Residues: 1588-2704, 1985
B; Cochemistry 24, 2698-2704, 1985
A; Reference number: A90495; MUID:85280409; PMID:2992573
A; Residues: 1594-2386 <-0>A; Residues: 1594-2389 <-0>A; Residues: 1594-2389 <-0>A; Residues: 1594-2
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A/Accession: A21166
B/Accession: A21298
A/Accession: A21398
A/Accession: A22398
A/Acce
            Reference number: A91008; MUID:85284965; PMID:2992939
                                                                                                                                       Status: nucleic acid sequence not shown
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A;Molecule type: protein
A;Residues: 291-300;551-560 <GAR2>
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Atjurtons 1917, 4941, 4242/3, 4494/3

C; Superfamily: fibronectin, fibronectin type I repeat homology; fibronectin type II repeat homology; fibronectin type II repeat homology; fibronectin type II adhesion; collagen binding; disulfide bond; duplowers alternative splicing; cell adhesion; collagen binding; disulfide bond; R; 1-32/Domain: signal sequence #status predicted <AIG>
F; 3-247/Product: fibronectin type I repeat homology <1F2>
F; 38-136/Domain: fibronectin type I repeat homology <1F2>
F; 187-226/Domain: fibronectin type I repeat homology <1F5>
F; 187-226/Domain: fibronectin type I repeat homology <1F5>
F; 308-342/Domain: fibronectin type I repeat homology <1F5>
F; 308-340/Domain: fibronectin type I repeat homology <2F2>
F; 470-68/Domain: fibronectin type II repeat homology <1F3>
F; 470-68/Domain: fibronectin type II repeat homology <1F9>
F; 518-555/Domain: fibronectin type II repeat homology <1F9>
F; 518-555/Domain: fibronectin type II repeat homology <1F9>
F; 518-559/Domain: fibronectin type III repeat homology <1F9>
F; 518-559/Domain: fibronectin type III repeat homology <1F9>
F; 518-599/Domain: fibronectin type III repeat homology <1F9
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C;Date: 31-Dec-1988 #sequence revision 31-Dec-1988 #text_change 09-Jul-2004
C;Accession: A26452; B21165; A22292
R;Skorstengaard, K.; Jensen, M.S.; Sahl, P.; Petersen, T.E.; Magnusson, S. Bur. J. Biochem. 161, 441-453, 1986
A;Title: Complete primary structure of bovine plasma fibronectin.
A;Reference number: A26452; MUID:87054047; PMID:3780752
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A;Cross-references: GB:M11750; NID:g204164; PIDN:AAA41170.1; PID:g554437
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A;Molecule type: protein
A;Residues: 1-2265 <8KO>
A;Cross-references UNLPROT:P07589
A;Kornblihtt, A.R.; Vibe-Pedersen, K.; Baralle, F.
Proc. Natl. Acad. Sci. U.S.A. 80, 3218-3222, 1983
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     translated from GB/EMBL/DDBJ
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A,Molecule type: mRNA
A,Residues: 1586-170, T',1722,1813-2477 <SC2>
R,Odermatt, E.; Tamkun, J.W.; Hynes, R.O.
Proc. Natl. Acad. Sci. U.S.A. 82, 6571-6575, 1985
A,Title: Repeating modular structure of the fibronectin gene: Relationship to protein st
A,Reference number: 159049; MUID:86016741; PMID:3863113
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A,Molecule type: DNA
A,Molecule type: DNA
A,Molecule type: DNA
A,Rosidues: 1-139,2382-2477 <PAT>
A,Cosdues: 1-139,2382-2477 <PAT>
A,Cosdues: 1-139,2382-2477 <PAT>
A,Cosdues: 1-139,2382-2477 <PAT>
A,Note: the authors translated the codon CCT for residues 51 and 94 as Ala
R,Schwarzbauer, J.E.; Tamkun, J.W.; Lemischka, I.R.; Hynes, R.O.
A,711-18: Three different fibronectin mRNAs arise by alternative splicing within the codi
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A; Residues: 1-2477 (4TN)
A; Residues: 1-2477 (4TN)
A; Residues: 1-2477 (4TN)
A; Cross-references: UNIPROT: P04937; EMBL: X15906; NID: g56163; PIDN: CAA34020.1; PID: g56164
R; Schwarzbauer, J.E.; Patel, R.S.; Fonda, D.; Hynes, R.O.
EMBO J. 6, 2573-2580, 1987
A; Title: Multiple sites of alternative splicing of the rat fibronectin gene transcript.
A; Reference number: S12455; MUID: 88054951; PMID: 2445560
A; Scatus: nucleic acid sequence not shown
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Aymolecule type: mmNA
By Command

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A;Molecule type: protein
A;Molecule type: protein
A;Molecule type: protein
A;Residues: 1183-1192;GLN',1268,'P',1270-1271,'D',1273,'CF',1276,'PY';1385-1399 <FAL>
R;Patel, R.S.; Odermatt, E.; Schwarzbauer, J.E.; Hynes, R.O.
EMBO J. 6, 2565-2572, 1987
A;Title: Organization of the fibronectin gene provides evidence for exon shuffling durib;Reference number: S00459; MUID:88054950; PMID:3119323
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Accession: S14428; S12455; Ā22319; S46203; S00459; A27252; I59049
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                                                                                                                                                                                                                                                                                                                                                          Length 2386;
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F;906-988/Domain: fibronectin type III repeat homology <3FD>F;996-1077/Domain: fibronectin type III repeat homology <3FE>F;1086-1164/Domain: fibronectin type III repeat homology <3FF>F;1108-11258/Domain: fibronectin type III repeat homology <3FF>F;1126-1349/Domain: fibronectin type III repeat homology <3FF>F)
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Pred. No. 1.7e-25;
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R;Hynee, R.O.
A;Bunitted to the EMBL Data Library, July 1989
A;Reference number: S14428
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Best Local Similarity 100.0%;

Matches 49; Conservative 0.
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Clomment: Partocenterin is synthesized by hepatocytes.

Clomment: Planam ilbrocentin is synthesized by hepatocytes.

Clomment: Planam ilbrocentin is synthesized by hepatocytes.

Clomment: Change and the context of the collagen binding; duplication; attracellu planam ilbrocentin type I repeat homology (173)

Fill-14(Pomain: Elbrocentin type I repeat homology (175)

Fill-15-14(Pomain: Elbrocentin type I repeat homology (175)

Fill-15-14(Pomain: Elbrocentin type I repeat homology (175)

Fill-14(Pomain: Elbrocentin type I repeat homology (177)

Fill-14(Pomain: Elbrocentin type I repeat homology (177)

Fill-14(Pomain: Elbrocentin type I repeat homology (177)

Fill-14(Pomain: Elbrocentin type II repeat homology (178)

Fill-14(Pomain: Elbrocentin type III repeat homology (178)

Fill-14(Fill-15(Pomain: Elbrocentin type III rep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,Molecule type: protein
A,Residues: 1-16, C'. 18-20, S'. 22-432,447-463;1367-1517;1567-1673;2062-2176, 'N', 2178-226
C;Comment: Cys-1201 and Cys-2015 have free sulfhydryl groups.
C;Comment: The plasma fibronectin molecule consists of two chains, which are connected by C;Comment: The plasma fibronectin soluding cell surfaces and various compounds including collagen, fib
                                                                                                                            A; Molecule type: mRNA

A; Residues: 2170-2265 < KOR>

A; Residues: 2170-2265 < KOR>

A; Cross-references: GB: KNO8800; NID:g163055; PIDN:AAA30521.2; PID:g5713323

R; Petersen, T.E.; Thogersen, H.C.; Skorstengaard, K.; Vibe-Pedersen, K.; Sahl, P.; Sottr

R; Petersen, T.E.; Thogersen, H.C.; Skorstengaard, K.; Vibe-Pedersen, K.; Sahl, P.; Sottr

R; Petersen, T.E.; Thogersen, H.C.; Skorstengaard, K.; Vibe-Pedersen, K.; Sahl, P.; Sottr

R; Petersen, T.E.; Thogersen, H.C.; Skorstengaard, K.; Vibe-Pedersen, K.; Sahl, P.; Sottr

A; Title: Partial primary structure of blowine plasma fibronectin: three types of internal

A; Reference number: A23292; MUID:83117805; PMID:6218503
    for human and bovine fibronecting
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Pred. No. 4.7e-23;
-----hes 2; Indels
    Title: Isolation and characterization of cDNA clones f
Reference number: A21165; MUID:83221567; PMID:6304699
characterization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          :2263/Binding site: phosphate (Ser)
                                                                                                 Accession: B21165
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Accession: A23292
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A;Residues: 1-2481 <DES>
A;Cross-references: GB:M77820
A;Cross-references: GB:M77820
C;Superfamily: fibronectin; fibronectin type I repeat homology; fibronectin type II repeat C;Keywords: duplication; extracellular matrix; glycoprotein; heterodimer
F;55-90/Domain: fibronectin type I repeat homology <IF:>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fib2-90/Domain: fibzonectin type I repeat homology <187>
Fib3-91-30/Domain: fibzonectin type I repeat homology <187>
Fil4-182/Domain: fibzonectin type I repeat homology <187>
Fil4-228/Domain: fibzonectin type I repeat homology <187>
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Fil40-228/Domain: fibzonectin type I repeat homology <187>
Fil40-258/Domain: fibzonectin type II repeat homology <187>
Fil40-556/Domain: fibzonectin type II repeat homology <187>
Fil40-693/Domain: fibzonectin type II repeat homology <187>
Fil40-693/Domain: fibzonectin type III repeat homology <187>
Fil40-693/Domain: fibzonectin type III repeat homology <187>
Fil40-693/Domain: fibzonectin type III repeat homology <1875>
Fil40-693/Domain: fibzonectin type III repeat homology <1873>
Fil40-1440/Domain: fibzonectin type III repeat homology <1873>
Fil40-1440/Domain: fibzonectin type III repeat homology <1873>
Fil40-1440/Domain: fibzonectin type III repeat homology <1873>
Fil40-1963/Domain: fibz
                               C;Species: Xenopus laevis (African clawed frog)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 12-Feb-1999
C;Accession: A49908
R;DeSimone, D.W.; Norton, P.A.; Hynes, R.O.
Dev. Biol. 149, 357-369, 1992
A;Title: Identification and characterization of alternatively spliced fibronectin mRNAs
A;Reference number: A43908; MUID:92111942; PMID:1730390
                                                                                                                                                                                                                                                                                                                                                      A,Accession: ^{A43908}
A,Status: nucleic acid sequence not shown; not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ï
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C;Species: Wus muscutlus (house mouse)
C;Date: 19-Dec-1993 #sequence revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A49173; A31371; G60597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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ilarity 71.4%;
Conservative 3
fibronectin - African clawed frog
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nes 35; Conser
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Gaps

ö 49

1 QAQQMVQPQSPVAVSQSKPGCYDNGKHYQINQQWERTYLGNVLVCTCYG

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Length 2265;

92.7%; 89.8%;

Query Match
Best Local Similarity 89.8
Matches 44; Conservative

<u>.</u> ز

Gaps

1;

11;

Length 1020;

DB 2;

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C;Species: Notophthalms viridescens, Triturus viridescens (eastern newt)
C;Species: Notophthalms viridescens, Triturus viridescens (eastern newt)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Accession: 151279
R;Nace, J.D.; Tassava, R.A.
Dev. Dyn. 202, 153-164, 1995
A;Title: Examination of fibronectin distribution and its sources in the regenerating neral reference number: 151279; MUID:95252528; PMID:7734733
A;Accession: 151279
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-190 <NAC.
A;Crose-references: UNIPROT:Q91400; GB:S76886; NID:g914305; PIDN:AAB34250.1; PID:g91430
C;Superfamily: fibronectin; fibronectin type I repeat homology <17-A8/Domain: fibronectin type I repeat homology <18-A8/Domain: fibronectin type I repeat homology <18-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17 SKPGCYDNGKHYQINQQWERT-YLGNVLVCTCYG 49
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Pred. No. 0.1;
8; Mismatches
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                                                                                                   28.9%;
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1 Similarity 31.9%;
15; Conservative 6
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Best Local Similarity 38...
Best Local Similarity
The second of the second
                                                                                                   Query Match
Best Local Similarity 41.2
Matches 14; Conservative
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Best Local Similarity
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Rivorton, P.A.; Hynes, R.O.
Mol. Cell. Biol. 7, 4297-4307, 1987

A;Title: Alternative splicing of chicken fibronectin in embryos and in normal and transf A;Title: Alternative splicing of chicken fibronectin in embryos and in normal and transf A;Title: Alternative splicing of chicken fibronectin in embryos and in normal and transf A;Title: Alternative splicing of chicken fibronectin in type II repeat homology; fibronectin type II repeat homology; fibronectin type II repeat homology cFN31>
R;180-262/Domain: fibronectin type III repeat homology cFN31>
F;180-262/Domain: fibronectin type III repeat homology cFN31>
F;257-259/Region: cell attachment (R.G-D) motif F;257-259/Region: cell attachment type III repeat homology cFN31>
F;257-259/Region: fibronectin type III repeat homology cFN31>
F;257-259/Region: fibronectin type III repeat homology cFN33>
F;257-259/Domain: fibronectin type III repeat homology cFN33>
F;246-628/Domain: fibronectin type III repeat homology cFN33>
F;240-979/Domain: fibronectin type III repeat homology cFN33>
F;240-979/Domain: fibronectin type III repeat homology cFN33>
F;240-959/Sc07-979/Domain: fibronectin type III repeat
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A,Status: nucleic acid sequence not shown
A,Status: nucleic acid sequence not shown
A,Status: nucleic acid sequence not shown
A,Status: nucleic acid sequence
C,Superfamily: fibronectin; fibronectin type I repeat homology, fibronectin type II repeat
C,Superfamily: fibronectin; fibronectin type I repeat homology <1F12>
F;11-46/Domain: fibronectin type I repeat homology <1F12>
F;11-46/Domain: fibronectin type I repeat homology <1F12>
F;11-46/Disulfide bonds: #status predicted
F;84/Disulfide bonds: interchain (to 88) #status predicted
F;88/Disulfide bonds: interchain (to 84) #status predicted
R; Khandjian, E.W.; Salomon, C.; Leonard, N.; Tremblay, S.; Turler, H.

Exp. Cell Res. 202, 464-470, 1992

A; Title: IRES. 202, 464-470, 1992

A; Title: IRES. 202, 464-470, 1992

A; Title: IRES. 202, 464-470, 1992

A; Reference number: A49173; MUID:93011702; PMID:337855

A; Recession: A49173

A; Rocession: A49173

A; Residues: L-103 «KHA»

A; Rigitues: L-104 «KHA»

A; Rigitues: L-104 «KHA»

A; Rigitues: L-105 «KHA»

A; Rigitues: L
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A; Residues: 1-65, 'N', 67-103 <BLA>
A; Residues: 1-65, 'N', 67-103 <BLA>
A; Cross-references: GB:M18194; GB:J03646; NID:g193329; PIDN:AAA37636.1; PID:g387159
R; Kyseck, R.P.; Macdonald-Bravo, H.; Zerial, M.; Bravo, R.
Exp. Cell Res. 180, 537-545, 1989
A; Title: Coordinate induction of fibronectin, fibronectin receptor, tropomyosin, and act
A; Reference number: A60597; MUID:89121031; PMID:2521606
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Species: Gallus gallus (chicken)
Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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51.7%; Pred. No. 1.9e-06;
ive 7; Mismatches 7; Indels
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Conservative
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Best Local Similarity
Matches 15; Conserv
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Length 190;

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Call 79, 779-79, 1994
R. Sasai, Y.; Lu, B.; Steinheisser, H.; Geissert, D.; Gont, L.K.; De Robertis, E.M.
R. Sasai, Y.; Lu, B.; Steinheisser, H.; Geissert, D.; Gont, L.K.; De Robertis, E.M.
Call 79, 779-79, 1994
A. Title: Xenopus chordin: a novel dorsalizing factor activated by organizer-specific ho
A. Reference number: A55195; MUD: 95094250; PMID: 8001117
A. A. Cassain. A55195
A. A. Cassain. A55195
A. Residence: L-941 - CASAS
A. Residues: L-941 - CASAS
A. Caross-references: UNIPROT: Q91713; GB: L35764; NID: g603944; PIDN: AAC42222.1; PID: g60394
C; Superfamily: chordin; von Willebrand factor type C repeat homology cVWC2>
F; 752-109, Domain: von Willebrand factor type C repeat homology cVWC2>
F; 770-640, Domain: von Willebrand factor type C repeat homology cVWC3>
F; 858-922, Domain: von Willebrand factor type C repeat homology cVWC3>
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                                                                                                                                                                                                                                                                                                                         chordin precursor - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
1;
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15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 57.5; DB 1; Length 9
Pred. No. 49;
6; Mismatches 21; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96 VAYSQLRDQCIVDGITYDVNHTFTKRHEEGHMMCTCYG 134
                                                                           12 VAVSQSKPGCYDNGKHYQINQQW-ERTYLGNVLVCTCYG
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hypothetical protein B - Shigella sonnei insertion sequence IS600
C;Species: Shigella sonnei
C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 09-Jul-2004
C;Accession: S03412
R;Matsutani, S.; Ohtsubo, H.; Maeda, Y.; Ohtsubo, E.
J. Mol. Biol. 196, 445-455, 1987
A;Title: Isolation and characterization of IS elements repeated in the bacterial chromos A;Reference number: S03411; MUID:88062685; PMID:2824781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tumm A; Reference number: A97359; MUID:21608551; PMID:11743194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: UNIPROT:Q8UHSO; GB:AE007869; PIDN:AAK86420.1; PID:g15155556; GSPDB:C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: UNIPROT:P16940; EMBL:X05952; NID:948667; PIDN:CAA29385.1; PID:948669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Agrobacterium tumefaciens
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C;Accession: C97433
C;Accession: C97433
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VVAPTSPFLARQIKAGVYQKLDKSKLPNLKNAWPDITERLAKYDPGNEYAVNYMWGTTGI 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        - Agrobacterium tumefaciens
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C;Superfamily: Escherichia coli spermidine/putrescine-binding protein
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F;194-534/Domain: glycine C-acetyltransferase homology <GCA> F;391/Binding site: pyridoxal phosphate (Lys) (covalent) #status
                                                                                                 Length 587;
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36;
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                                                                                                                                                                 Mismatches
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Pred. No. 20;
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Pred. No. 26
                                                                                                 Score 57;
Pred. No.
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563 HFELMSEWERSYFGNM 578
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                                                                                                                                                                                                                                 42
                                                                                              20.7%;
ilarity 43.8%;
Conservative
                                                                                                                                                                                                                                 27 HYQINQQWERTYLGNV
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                                                                   Query Match
Best Local Similarity
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Best Local Similarity
Matches 15; Conserv
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A,Molecule type: DNA
A,Residues: 1-365 <KUR>
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A; Residues: 1-272 <MAT>
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                                                                                                                                                                                                                                 Apaccession: A29040
Apacces: 1-586 <SCH
Apacces: UNIPROT: D08680; GB:M15268; NID:g191857; PIDN:AAA37207.1; PID:g387096
Apacterin Sci. 2, 1959-1965, 1993
Apacterin Sci. 2, 1959-1966, 1993
Apacterin Sci. 2, 1959-1966
Apacterin Sci. 2, 1959
Apacte
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A,Status: preliminary
A,Molecule type: mRNA
A,Cross-references: UNIPROT: P22557; EMBL: X60364; NID: 928587; PIDN: CAA42916.1; PID: 928588
A,Note: the sequence from Fig. 4 is inconsistent with that from Fig. 2 in having 147-Leu
R,Note: the sequence from Fig. 4 is inconsistent with that from Fig. 2 in having 147-Leu
R, Bishop, D.F.
Nucleic Acids Res. 18, 7187-7188, 1990
A,Title: Two different genes encode delta-aminolevulinate synthase in humans: nucleotide
A,Reference number: S13682; MUID: 91088347; PMID: 2263504
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A;Title: Nucleotide sequence of mouse 5-aminolevulinic acid synthase cONA and expression A;Reference number: A29040; MUID:87163516; PMID:3557128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5-aminolevulinate synthase (EC 2.3.1.37) precursor, erythroid-specific, mitochondrial - N;Alternate names: 5-aminolevulinate synthase 2; erythroid delta-aminolevulinate synthas C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 21.Nov-1993 #sequence_revision 06-Sep-1996 #text_change 09-Jul-2004
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F;330/Binding site: pyridoxal phosphate (Lys) (covalent) #status experimental
                                 Species: Mus musculus (house mouse)
Date: 30-Jun-1990 #sequence revision 30-Jun-1990 #text change 09-Jul-2004
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Pred. No. 36;
   names: delta-aminolevulinate synthase, nonspecific
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562 HFELMSEWERSYFGNM 577
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                                                                                          Accession: A29040; Schoenhaut, D.S.; Curtis, P.J.
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Best Local Similarity
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A;Cross-references: UNIPROT:Q19780; EMBL:U50197; PIDN:AAA91255.1; CESP:F25E2.2
A;Experimental source: strain Bristol N2
C;Genetics:
A;Gene: (CESP:F25E2.2
A;Introns: 54/1; 94/1; 154/1; 179/3; 209/1; 249/1; 321/1; 422/1; 551/2; 623/1
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T29818
A;Reference number: 220691
A;Reference number: 220691
A;Accession: T29918
A;Accession: T29918
A;Accession: T29918
A;Molecule type: DNA
A;Residues: 1-645 <MINA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 20.0%; Score 55, DB 2, Length 645; Best Local Similarity 38.5%; Pred. No. 70; Matches 10; Conservative 3; Mismatches 13; Indels
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R; Bevan, M.; Lennard, N.; Quail, M.; Harris, B.; Rajandream, M.A.; Barrell, B.G.; Bancro submitted to the Protein Sequence Database, June 1999
A; Reference number: Z16533
A; Rocession: T10544
A; Molecule type: DNA
A; Residues: 1-338 < BEV>
A; Residues: 1-338 < BEV>
A; Residues: 1-338 < BEV>
A; Residues: L338 < BEV>
A; Experimental source: cultivar Columbia; BAC clone T12G13
A; Experimental source: cultivar L311; 175/1; 215/1; 274/1; 292/3
                                                                                                                                                                                                                                                                                       C;Accession: AD2651
R;Wood, D.W.; Seubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I. K.; Kood, D.W.; Seubal, J.C.; Kaul, R.; Monks, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A, Status: preliminary
A, Rolecule type: DNA
A, Rosidues: 1-365 «KUR»
A, Cross-references: UNIPROT: Q8UHSO; GB: AE008688; PIDN: AAL41626.1; PID: g17738965; GSPDB:C
B, Experimental source: strain C58 (Dupont)
A, Gene: pot
                                                                                                                                                                                                     - Agrobacterium tumefaciens (strain C58, Dupont)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ster, E.W.

A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A;Reference number: AB2577; MUID:21608550; PMID:11743193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    inositol 1,3,4-trisphosphate 5/6-kinase homolog T12G13.10 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1;
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                                                                                                                                                                                                                            Species: Agrobacterium tumefaciens
Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels 25; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Map position: circular chromosome
C;Superfamily: Escherichia coli spermidine/putrescine-binding protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20.5%; Score 56.5; DB
24.6%; Pred. No. 26;
Live 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ||: |:|| | ::| | VAIDQNKPLSEQGPFDIVLHKQIGKEWRR 100
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                                                                                                                                                                                                     hypothetical protein potf [imported]
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Best Local Similarity 24.6'
Matches 15, Conservative
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RESULT 15 T29818 hypothetical protein P25E2.2 - Caenorhabditis elegans

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oryctolagus
bos taurus
canis famil
equus cabal
                                                                                                                                      gállus gall
notophthalm
anopheles g
ambystoma m
homo sapien
oryctolagus
pleurodeles
                                                              brachydanio
                                              bos taurus
                                                                                                                                                                                                   drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PERFORMANCE FROM N.A.

TISSUBERER FROM N.A.

TISSUBERER FROM N.A.

BIOCCKET H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,

A Bloccker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,

A Bloccker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,

A Blocker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,

A Blocker H. B. Mewes H.W., Weil B., Amid C., Osanger A.,

B COD G., Han M., Wiemann S.;

R EMBL, BX538045; CAD97984.1; -.

R EMBL, BX538045; CAD97984.1; -.

R GO, GO.005576; C.extracellular; IEA.

R GO, GO.0005576; C.extracellular; IEA.

R HESP, OSONO5576; FN_TYPE_II.

R FAM, PROMO406, fn2; 2.

R FAM, PROMO406; fn2; 2.

R PROMO406; FN2; 2.

R MART; SW00058; FN2; 2.

R PROSITE; PS00022; FRF; 1, UNKNOWN 1.

R PROSITE; PS00023; FIBRONECTIN_1; 9.

R PROSITE; PS00023; FIBRONECTIN_2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QGMZF4;
05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein DKFZp686Ki39 (Hypothetical protein DKFZp686F219)
(Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           124 QAQQMVQPQSPVAVSQSKPGCYDNGKHYQINQQWERTYLGNALVCTCYG 172
                           Length 749;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 QAQQMVQPQSPVAVSQSKPGCYDNGKHYQINQQWERTYLGNVLVCTCYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  749 AA; 83524 MW; C8DDF97F3ED2F0DE CRC64;
                                                                                                                                                                                                                                                                                                                          Q72391 PRELIMINARY; PRT; 749 AA. Q72391; 01-0CT-2003 (TYENBLrel. 25, Created) 01-0CT-2003 (TYENBLrel. 25, Last sequence update) 01-MAR-2004 (TYENBLrel. 26, Last annotation update) Hypothetical protein DKFZp686B18150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 271; DB 2;
Pred. No. 3.7e-25;
0; Mismatches 1;
                                                                                                                                                                                                                                                  ALIGNMENTS
              602816
FONC PLEWA
Q95KV5
O772W7
C9712W7
Q95KV4
FINC CANFA
FINC CANFA
FINC CHICK
FINC OTVI
G970KK5
G970KC5
Q970KC5
Q970KC5
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Best Local Similarity 98.0%;
Matches 48; Conservative
2193
1328
1328
347
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62
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1256
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141
141
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SEQUENCE 749 AA; 8
                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human)
 NCBI_TaxID=9606
 110
103.5
82.5
82.5
80.5
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80.5
67.5
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Q6MZF4
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 Q7Z391
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                                                                                                        52 ; Search time 35.4502 Seconds (without alignments) 707.807 Million cell updates/sec
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                5.1.6
Compugen Ltd.
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                                                                                                                                                                                                                                                                               1612378 segs, 512079187 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUMMARIES
                GenCore version
Copyright (c) 1993 - 2005
                                                                                                          September 30, 2005, 13:30:52
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FINC MOUSE
O68DP8
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FINC BOVIN
FINC XENLA
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FINC RABIT
Q862C9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FINC HUMAN
Q6N025
Q6MZU5
Q6BDP9
                                                                                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                           - protein search, using sw model
                                                                                                                                                                   US-09-492-971B-15_COPY_4_52
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Q6N0A6
Q68DT4
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Q7L553
Q99KD0
Q6PJE5
Q71U44
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Q6MZS0
Q68CX6
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Gapop 10.0 , Gapext 0.5
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1: uniprot_sprot:*
2: uniprot_trembl:*
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length: 2000000000
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Match Length DB
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Minimum DB 8

Database

Perfect score:

Sequence:

OM protein

Run on:

Scoring table:

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271 271 271 271 271 263 263 263 264 264 194 194 117 117 117 117

Score

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Result

; 0

Gaps

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The German cDNA Consortium;

A Koehrer K., Beyer A., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;

B Fobo G., Han M., Wiemann S.;

Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.

R InterPro; IPR002086; Aldehyd dehydrog.

R InterPro; IPR002083; FibIntchl.

R InterPro; IPR003952; FMIII_subd.

R Figh; PF000049; FMIII_12.

R Ffam; PF000040; FMI; 12.

R Ffam; PR000041; FMIYPEII.

R PRINTS; PR00013; FMIYPEII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32 QAQQMVQPQSPVAVSQSKPGCYDNGKHYQINQQWERTYLGNALVCTCYG 80
                                                                                                                                                                                                                                                                                                                                                                 98.5%; Score 271; DB 2; Length 2296; 98.0%; Pred. No. 1.2e-24; arive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2; Length 2357;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 QAQQMVQPQSPVAVSQSKPGCYDNGKHYQINQQWERTYLGNVLVCTCYG
                                                                                                                                                                                                                                                                                                                             2296 AA; 252761 MW; 9AB2D723CC0CED70 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Hypothei.cal protein DKFZp686F10164.
Name=DKFZp686F10164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Prodom; PD000995; FN TYPE_II; 2.
SWART; SW00059; FN1; 12.
SWART; SW00069; FN2; 2.
SWART; SW00060; FN2; 15.
PROSITE; PS00687; ALDEHYDE DEHYDR GLU; UNKNOWN_1.
PROSITE; PS010223; FIERONECTIN 1; 12.
PROSITE; PS01023; FIERONECTIN 2; 2.
                                                                                                                                                                                               PROSITE; PS00667; ALDEHYDE DEHYDR GLU; UNKNOWN_1.PROSITE; PS00022; EGF 1; UNKNOWN 2.PROSITE; PS01023; EGF 1; UNKNOWN 2.PROSITE; PS01023; FIBROMECTIN 1; 12.PROSITE; PS0593; FIBROMECTIN_2; 2.PROSITE; PS5693; FM3; 15.PROSITE; PS5693; FM3; 15.PROSITE; PS56943; Z52761 MW; 9AB2D723CCOCED70
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                                                                        PRINTS; PRO0012; FNTYPEI.
PRINTS; PR00013; FNTYPEII.
ProDom; PD000995; FN TYPe_II; 2.
SMART; SM00058; FNI; 12.
SMART; SM00059; FN2; 2.
SMART; SM00060; FN3; 15.
InterPro; IPR000562; FN_Type_II
                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 98.0 Matches 48; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
TISSUE=Uterus endothel;
                 Pfam; PF00039; fn1; 12.
Pfam; PF00040; fn2; 2.
Pfam; PF00041; fn3; 15.
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2357 AA; 2
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SEQUENCE 23
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                                                                                                                                   TISSUE-Human cervix;
The German Human cDNA Consortium;
Ansorge W., Krieger S., Regiert T., Rittmueller C., Schwager B.,
Mewes H.W., Weil B., Amid C., Osanger A., Pobo G., Han M., Wiemann S.;
Submitred (Aug-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; Bx649182; CAE42200.1;
EMBL; Bx640802; CAE45885.1;
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Blocker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;

Fobo G., Han M., Wiemann S.;

Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.

EMBL; BX640608; CAB45714.1;

GQ; GQ:005576; C:extracellular; IEA.

InterPro; IPR006209; EGF like.

InterPro; IPR006209; EGF like.

InterPro; IPR000396; Aldehyd dehydrog.

InterPro; IPR000396; INIII.

InterPro; IPR008957; FN_III.
                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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98.0%; Pred. No. 5.6e-25;
tive 0; Mismatches 1; Indels
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SEQUENCE 1103 AA; 122113 MW; 82FEC4CAF634AD56 CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein DKFZp686M04163.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Human uterus endothel primary cell culture;
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Name=DKFZp686K139; Synonyms=DKFZp686F219;
                                                                                                                                                                                                                                                                          GG, GG:0005576; CARATAGGILLIAR; IEA.
InterPro; IPR006209; EGF_like.
InterPro; IPR006209; EGF_like.
InterPro; IPR001895; Fibrnctn1.
InterPro; IPR001895; FN III-like.
InterPro; IPR001895; FN III-like.
InterPro; IPR001895; FN III-like.
Pfam; PF00040; fn2; 2.
Pfam; PF00041; fn3; 4.
PRINTS; PR00013; FNTYPEI.
PROPOM; PD000995; FN TYPEII.
ProDom; PD000995; FN TYPEII.
ProDom; PD000995; FN TYPEII; 2.
SMART; SM00060; FN3; 4.
SMART; SM00060; FN3; 4.
PROSITE; PS00022; EGF 1; UNKNOWN I.
PROSITE; PS01253; FIBRONECTIN 1; 9.
PROSITE; PS01253; FIBRONECTIN 1; 9.
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nes 48; Conservative
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                     Homo sapiens (Human)
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RESULT 3

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human fibronectin gene

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=84272258; PubMed=6462919; Kornblihtt A.R., Vibe-Pedersen K., Baralle F.E.; Kornblihtt A.R., Vibe-Pedersen K., Baralle F.E.; Human fibronectin: cell specific alternative mRNA splicing generates polypeptide chains differing in the number of internal repeats."; Nucleic Acids Res. 12:5853-5868(1984).
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                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=21600194; PubMed=11737888; DOI=10.1186/bcr325; Schor S.L., Schor A.M.; Phenotypic and genetic alterations in mammary stroma: implications
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=87030890; PubMed=3770189; DOI=10.1016/0014-5793(86)80029-1; Gutman A., Yamada K.M., Kornblihtt A.R.; "Human fibronectin is synthesized as a pre-propolypeptide."; FEBS Lett. 207:145-148(1986).
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                               FINC HUMAN STANDARD; PRT; 2386 AA.
P02751; 095609; 095610; 014312; 014325; 014326; 086T27; Q8IVI8; 096KP9; 0956809; 094RP3; Q9HMK2; 021-UUJ-1986 (Rel. 01, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
25-CTT-2004 (Rel. 45, Last annotation update)
Fibronectin precursor (FN) (Cold-insoluble globulin) (CIG).
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MEDLINE=85284965; PubMed=2992939;
Kornblihtt A.R., Umezawa K., Vibe-Pedersen K., Baralle F.E.;
"Primary structure of human fibronectin: differential splicing igenerate at least 10 polypeptides from a single gene.";
EMBO J. 4:1755-1759(1985).
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                                                                                     124 QAQQWVQPQSPVAVSQSKPGCYDNGKHYQINQQWERTYLGNALVCTCYG 172
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                                                                1 QAQQMVQPQSPVAVSQSKPGCYDNGKHYQINQQWERTYLGNVLVCTCYG
                       Indels
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Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ansorge W., Krieger S., Regiert T., Rittmueller C.,
Mewes H.-W., Weil B., Amid C., Osanger A., Fobo G.,
Pred. No. 1.2e-24;
); Mismatches 1;
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98.0%;
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                    Conservative
                                                                                                                                                                                                                                                                                                                                                                            Name=FN1; Synonyms=FN;
Homo sapiens (Human).
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Similarity
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Best Local
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MEDLINE=87026578; PubMed=3021206;
Sekiguchi K., Klos A.M., Kurachi K., Yoshitake S., Hakomori S.;
"Human liver fibronectin complementary DNAs: identification of two
different messenger RNAs possibly encoding the alpha and beta subunits
of plasma fibronectin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                            P.A.;
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Garcia-Pardo A., Pearlstein E., Frangione B.;
"Primary structure of human plasma fibronectin. The 29,000-dalton NH2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 309-608, AND COLLAGEN-BINDING.
MEDLINE=87080265; PubMed=3024962;
Owens R.J., Baralle F.E.;
"Mapping the collager-binding site of human fibronectin by expression in Escherichia coll.";
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domains separated by
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Liu M.C., Yu S., Sy J., Redman C.M., Lipmann F.;
"Tyrosine sulfation of proteins from the human hepatoma cell line
                                                                                                                                                                                                                                                                                                                                                                                                               MEDINE-82265664; PubMed=7050098; Perschaacher M.D., Ruoslahti E., Sundelin J., Lind P., Peterson "The cell attachment domain of fibronectin. Determination of the
                                                                                                                                     SEQUENCE OF 1257-1365 FROM N.A. (ISOFORM 11).
MEDLINE=88041070; PubMed=3478690;
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MBDLINB=22126816; PubMed=12127832; DOI=10.1053/joca.2002.0792;
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MEDLINE-85280409; PubMed-2992577;
Bernard M.P., Kolbe M., Weil D., Chu M.-L.;
"Human cellular fibronectin: comparison of the portion with rat identifies primary structural hypervariable regions.";
splicing of ED-B and ED-A regions of the
independent events.";
                                                              Nucleic Acids Res. 16:3545-3557(1988).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       domain.";
J. Biol. Chem. 261:2113-2116(1986).
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PubMed=9501082; DOI=10.1093/emboj/17.6.1606;

Sasaki T., Brakebusch C., Engel J., Timpl R.;

"Mac-2 binding protein is a cell-adhesive protein of the extracellular matrix which self-assembles into ring-like structures and binds betal integrins, collagens and fibronectin.";

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MEDLINE=93015879; PubMed=1400330;
Balbona K., Tran H., Godyna S., Ingham K.C., Strickland D.K.,
Argraves W.S.;
"Fibulin binds to itself and to the carboxyl-terminal heparin-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-95081153; PubMed=7989369;
Rosteagno A., Williams M.J., Baron M., Campbell I.D., Gold L.I.;
"Further characterization of the NH2-terminal fibrin-binding site on
fibronectin.";
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Potts J.R., Phan I., Williams M.J., Campbell I.D.;
"High-resolution structural studies of the factor XIIIa crosslinking site and the first type I module of fibronectin.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=93046665; PubMed=1423622; DOI=10.1016/0092-8674(92)90600-H; Main A.L., Harvey T.S., Baron M., Boyd J., Campbell I.D.; "The three-dimensional structure of the tenth type III module of the ibronectin: an insight into RGD-mediated interactions."; Cell 71:671-678(1992).
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Shively J.E., Pande H.;
Human plasma fibronectin. Demonstration of structural differences
between the A- and B-chains in the III CS region.";
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Williams M.J., Phan I., Harvey T.S., Rostagno A., Gold L.I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 2386;
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MEDLINE-92162710, PubMed=1311202,
Baron M., Main A.L., Driscoll P.C., Mardon H.J., Boyd J.,
Campbell I.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Match 98.5%; Score 271; DB 1; Length 23 Local Similarity 98.0%; Pred. No. 1.2e-24; les 48; Conservative 0; Mismatches 1; Indels
                        oc. Natl. Acad. Sci. U.S.A. 82:7160-7164(1985)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHARACTERIZATION OF FIBRIN-BINDING SITE 1.
                                                                                                                                                                                                                                                                                                                                                                                                                           region of fibronectin.";
J. Biol. Chem. 267:20120-20125(1992).
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                                                                                                      MEDLINE=91190085; PubMed=2012601;
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                                                                             O-GLYCOSYLATION OF THR-2064
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  HepG2."
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The German Human cDNA Consortium;
The German Human cDNA Consortium;
Poustka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R.,
Mewes H.W., Well B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;
Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BX640731; CAB45847.1; -.
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The German Human cDNA Consortium;
Bloecker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein DKFZp68601166.
                                                                                                                               05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein DKFZp686M2451 (Fragment).
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PROSITE; PSO1022; BGF 1; UNKNOWN 2.
PROSITE; PSO1022; FIBRONECTIN 1; 12.
PROSITE; PSO0023; FIBRONECTIN 2; 2.
PROSITE; PS50853; FN3; 16.
Hypothetical protein.
             PRT; 2444 AA.
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Interpro; IPR008957; FN_III-11ke.
Interpro; IPR000562; FN_IYPe_II.
Pfam; PF00039; fn1; 12.
Pfam; PF00040; fn2; 2.
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PROD0m; PD000995; FN_TYPE_II; 2.
SMART; SM00059; FN1; 12.
SMART; SM00059; FN2; 2.
SMART; SM00069; FN3; 16.
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Matches

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Mus musculus (Mouse)
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Q8C6J7
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Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.

EMBL; CR749316; CAH18171.1; -..

R InterPro; IPR002086; Aldehyd dehydrog.

R InterPro; IPR000209; EGF_like.

R InterPro; IPR00039; Fibinctnl.

R InterPro; IPR003961; FNIII subd.

R InterPro; IPR003961; FNIII subd.

R InterPro; IPR000391; FNIII subd.

R InterPro; IPR000395; FNIII subd.

R InterPro; IPR000395; FNIII-like.

R Pfam; PF00040; fn2; 2.

R Pfam; PF00040; fn2; 2.
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Mammalia, Eutheria, Primates, Catarrhini; Hominidae, Homo.
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                                                                                                                                                                                                                                                                                             98.5%; Score 271; DB 2; Length 2477; 98.0%; Pred. No. 1.3e-24; ive 0; Mismatches 1; Indels
Fobo G., Han M., Wiemann S.;
Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
BMBL; MX404075; CZR55932.1; --
GO; GO:0005576; C:extracellular; IEA.
InterPro; IPR002086; Aldehyd dehydrog.
InterPro; IPR002099; FDPInctnl.
InterPro; IPR000083; Fibrnctnl.
InterPro; IPR000557; FN III-like.
InterPro; IPR000557; FN III-like.
InterPro; IPR000562; FN III-like.
FRam; PP00040; fn1; 12.
Pfam; PP00040; fn1; 12.
Pfam; PP00041; fn3; 17.
                                                                                                                                                                                                                                                                          272335 MW; D358D85C6B18207C CRC64;
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25-0CT-2004 (TrEMBLrel. 28, Last sequence update)
25-0CT-2004 (TrEMBLrel. 28, Last annotation update)
Hypothetical protein DKFZp686K08164.
                                                                                                                                                                              SMART; SM00059; FN2; 2.
SMART; SM00060; FN3; 17.
PROSITE; PS00687; ALDEHYDE DEHYDR GLU; UNKNOWN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                          PRT; 2267 AA
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PRINTS; PR00013; FNTYPEII.
PRINTS; PR00014; FNTYPEIII.
ProDom; PD000995; FN Type_II; 2.
SMART; SM00059; FNI; 12.
SMART; SM00069; FNI; 12.
                                                                                                                                             PRINTS; PRO0013; FNTYPEII.
ProDom; PD000995; FN Type II; 2.
SMART; SM00058; FN1; 12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The German cDNA Consortium;
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                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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TISSUE=Uterus endothel;
                                                                                                                                                                                                                                                                        2477 AA;
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                                                                                                                                                                                                                                                                                                           Best Local Similarity
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SEQUENCE FROM N.A.
STRAINE-2059L6.07 IISSUE=Ovary;
STRAINE-20499374; PubMed=11042159; DOI=10.1101/gr.145100;
CARTHING: P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
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STRANIE-STBL/GJ IISSUB=Ovary;
The FANTOM CONSORTIUM.
THE RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
Manalysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
Nature 420:563-573 (2002).
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STRAIN=C57BL/6J; TISSUE=Ovary;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus 2 days pregnant adult female ovary cDNA, RIKEN full-
length enriched library, clone:E330027109 product:fibronectin 1, full
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MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
Shibate K., Itoh M., Alzawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watchiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.; "RIKEN integrated sequence analysis (RISA) system-384-format
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Ovary;
STRAIN=21085660; PubMed=11217851; DOI=10.1038/35055500;
RIKEN FANTOM CONSOrtium;
"FURCH FANTOM CONSOrtium of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
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PROSITE; PS00687; ALDEHYDE DEHYDR GLU; UNKNOWN_1.
PROSITE; PS00022; EGF 1; UNKNOWN 2.
PROSITE; PS01223; FIBRONECTIN 1; 12.
Hypothetical protein.
SEQUENCE 2267 AA; 249359 MW; C4D124A038C323DF CRC64;
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95.9%;
                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 95.93
Matches 47; Conservative
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Proc. Natl. Acad.
  CDNA
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MEDINE-2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
XRAINE-2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,
Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,
A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A Diatchenko L., Warusina K., Farmer A.A., Rubin G.M., Hong L.,
A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
A Roback S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
A Richards S.W. Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Richards S.W. Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Hilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A Hakealey R.W., Touchman J.W., Green B.D., Dickson M.C.,
Blakealey R.W., Touchman J.W., Green B.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skalksu U., Smailus D.E.,
Butterfield Y.S.N., Krzywinski M.I., Skalksu U., Smailus D.E.,
Generation and initial analysis of more than 15,000 full-length human
                                                                SEQUENCE FROM N.A.

STRAIN-CSTBL/6J; TISSUE-OVATY;
Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
Rukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
Adachi J., Aizawa K., Hanagaki T., Hara A., Hashizume W.,
Hayashida K., Hayatsu N., Hiramotco K., Hiraoka T., Hirozane T.,
A Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
A Hori F., Imotani Y., Cojima Y., Kondo S., Konno H., Kouda M., Koya S.,
Kurihara C., Mateuyama T., Miyazaki A., Murata M., Nakamura M.,
Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Oksato N.,
Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
M. Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
Submitted (UUL-2001) to the EMBL/GenBank/DDBJ databases.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
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sequencing pipeline with 384 multicapillary sequencer.";
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PROSITE; PS00022; EGF I. UNKNOWN 1.
PROSITE; PS01253; FIRRONECTIN 1; 5.
SEQUENCE 296 AA; 32617 MW; AOFFSF4809FB6439 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ch 95.6%; Score 263; DB 2;
1. Similarity 93.9%; Pred. No. 1.4e-24;
46; Conservative 2; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P11276; Q61567; Q61568; Q61569; Q64233; Q80UI4; 01-UUL-1989 (Rel. 11, Created) 29-WAR-2004 (Rel. 43, Last sequence update) 25-G77-2004 (Rel. 45, Last annotation update) Fibronectin precursor (FN).
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InterPro; IPR006209; BGF like.
InterPro; IPR000083; Fibrnctn1.
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HSSP; Q96KP7; 1FBR.
                       Genome Res. 10:1757-1771(2000)
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DOWN-REGULATION BY GLUCOCORTICOIDS.
MEDLINE=21600963; PubMed=11737251;
MEDLINE=21600963; PubMed=11737251;
GLU Y.-C., Talles J.F., Gullberg D., Timpl R., Ekblom M.;
Glucocorticoids down-regulate the extracellular marrix proteins fibronectin, fibulin-1 and fibulin-2 in bone marrow stroma.";
Eur. J. Haematol. 67.176-184 (2001).
-1- HAEMATON: Fibronectins fibrin, heparin, DNA, and actin. Fibronectins are involved in cell adhesion, cell motility, opsonization, wound healing, and maintenance of cell shape.
-1- SUBUNI: Mostly heterodimers or multimers of alternatively spliced variants, connected by 2 disulfide bonds near the carboxyl ends;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Talts J.F., Weller A., Timpl R., Ekblom M., Ekblom P.; "Regulation of mesenchymal extracellular matrix protein synthesis by transforming growth factor-beta and glucocorticoids in tumor stroma."; J. Cell Sci. 108:2153-2162(1995).
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MEDLINE=98202578; PubMed=9533887; DOI=10.1006/jmbi.1998.1616;
Copie V., Tomita Y., Akiyama S.K., Aota S., Yamada K.M., Venable R.M.,
Pastor R.W., Krueger S., Torchia D.A.;
"Solution structure and dynamics of linked cell attachment modules of
mouse fibronectin containing the RGD and synergy regions: comparison
with the human fibronectin crystal structure.";
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TISSUE SPECIFICITY: Plasma FN (soluble dimeric form) is secreted by hepatocytes. Cellular FN (dimeric or cross-linked multimeric forms), made by fibroblasts, epithelial and other cell types, is deposited as fibrils in the extracellular matrix.
INDUCTION: Glucocorticoids suppressed mRNA expression and protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              to a lesser extend homodimers. Interacts with FBLN1 and LGALS3BP (By similarity).
                                                                                                                                                                                                                                                               Polly P., Nicholson R.C.; "Sequence of the mouse fibronectin-encoding gene promoter region."; Gene 137:353-354(1993).
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Comment=A number of isoforms are produced. Each of the "extra
domain" and the connecting strand 3 are present in some forms
fibronectin and absent in others;
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MEDLINE=93011702; PubMed=1327855;
Khandjian E.W., Salomon C., Leonard N., Tremblay S., Turler H.;
Khrod-tin gene expression in proliferating, quiescent, and SV40-infected mouse kidney cells.";
Exp. Cell Res. 202:464-470(1992).
                                                                                                                                                                                                                       MEDLINE=94131313; PubMed=8299972; DOI=10.1016/0378-1119(93)90036-3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-88124987; PubMed-3124113;
Blatti S.P., Foster D.N., Ranganthan G., Moses H.L., Getz M.J.;
"Induction of fibronectin gene transcription and mRNA is a primary
response to growth-factor stimulation of AKR-2B cells.";
Proc. Natl. Acad. Sci. U.S.A. 85:1119-1123(1988).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gorski G., Aros M., Norton P.;
Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases
sequences.";
ad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=95403556; PubMed=7673336;
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TISSUBLEARY golds.

The German cDNA Consortium;

G The German cDNA Consortium;

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B COSTREARY STATES CANABLA CONSORTIANT CONSORTIANT
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Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Fibronectin type-III 11.
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Fibronectin type-III 16.
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Fibronectin type-III 17.
Fibronectin type-II 17.
Fibronectin type-II 17.
Fibronectin type-I 11.
Fibronectin type-I 12.
Cell attachment site.
Gell attachment site.
By similarity.
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PRINTS; PR00013; FWTYPEII.
PRINTS; PR00014; FWTYPEII.
PRODON; PD000095; FN TYPEIII.
SWART; SM00059; FN TYPEII.
SWART; SM00059; FN TYPEII.
SWART; SM00069; FN3: 12.
SWART; SM00069; FN3: 12.
PROSITE; PS00687; ALDEHYDE DEHYDR GLU; UNKNOWN_I.
PROSITE; PS01022; PSEF 1; UNKNOWN_Z.
PROSITE; PS01023; FIBRONECTIN 1; 10.
PROSITE; PS01023; FIBRONECTIN 2; 2.
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Hypothetical protein DKFZp686H0342.
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Matches 46; Conservative
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                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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PROSTER; PROBLES; PRISONECTIN 2; 2.

PROSTER; PROBLES; PAS, 17.

Glycoprotein; Heparin-binding; Phosphorylation; Plasma; Repeat; Signal; Sulfation.

SIGNAL 33 2477 Fibronectin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; 222729; CAA57796.1; --
REMBL; X22729; CAA57796.1; --
REMBL; X91402; CAA57796.1; --
REMBL; X91402; CAA57796.1; --
REMBL; X91402; AA8237636.1; --
REMBL; S45680; AA823491.1; --
REMBL; S45680; REMBL; G=1446-1630.
REMBL; MRR; G=1446-1630.
REMBL; MRR;
    synthesis.
--- PTM: Sulfated (By similarity).
--- SIMILARITY: Contains 12 fibronectin type I domains.
--- SIMILARITY: Contains 2 fibronectin type II domains.
--- SIMILARITY: Contains 17 fibronectin type III domains.
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Fibronectin.
Fibrin- and heparin-binding
Collagen-binding.
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Fibronectin type-1 3.
Fibronectin type-1 4.
Fibronectin type-1 5.
Fibronectin type-1 6.
Fibronectin type-1 1 1.
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Fibronectin type-1 7.
Fibronectin type-1 7.
Fibronectin type-1 9.
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Fibrin-binding 2
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InterPro; IPR00083; Fibrnctnl.
InterPro; IPR003962; Full subd.
InterPro; IPR003961; FN III.
InterPro; IPR008957; FN III.
InterPro; IPR008562; FN III.-like.
InterPro; IPR000852; FN III.-like.
Pfam; PF00049; fnl; 12.
Pfam; PF00040; fnl; 12.
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Biochem. J. 301:745-751(1994).
-!- FUNCTION: Fibronectins bind cell surfaces and various compounds including collagen, fibrin, heparin, DNA, and actin. Fibronectins
                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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                                                                                                      Gaps
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MEDLINE=84082067; PubMed=6317187; DOI=10.1016/0092-8674(83)90175-7; Schwarzbauer J.E., Tamkun J.W., Lemischka I.R., Hynes R.O.; Three different fibronectin mRNAs arise by alternative splicing within the coding region."; Cell 35:421-431(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-88054951; PubMed=2445560;
Scwarzbauer J.E., Patel R.S., Fonda D., Hynes R.O.;
"Multiple sites of alternative splicing of the rat fibronectin gene
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"A single rat fibronectin gene generates three different mRNAs
alternative splicing of a complex exon.";
Proc. Natl. Acad. Sci. U.S.A. 81:5140-5144(1984).
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                                                              Length 2240;
                                                                                                                                                                32 QAQQMVQPQSPVAVSQSKPGCYDNGKHYQINQQWERTNLGNALVCTCYG
                                                                                                                                           1 QAQQMVQPQSPVAVSQSKPGCYDNGKHYQINQQWERTYLGNVLVCTCYG
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Falkenberg C., Enghild J.J., Thogersen I.B., Salvesen G.,
Akerstrom B.;
                                                                                                    Indels
                    2240 AA; 246667 MW; 8FCDAF406F330621 CRC64;
                                       Score 262; DB 2; Le
Pred, No. 1.5e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         procein structure and subunit variation."; Proc. Natl. Acad. Sci. U.S.A. 82:6571-6575(1985)
                                                                                                                                                                                                                                                                                                 P04937; Q6LDX9;
13-AUC-1987 (Rel. 05, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
Fibronectin precursor (FN).
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                                                                                                    0; Mismatches
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MEDLINE=88054950; PubMed=3119323;
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                                                          95.3%;
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                                             Query Match
Best Local Similarity 95.9'
                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                            Rattus norvegicus (Rat).
    protein.
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Hypothetical
SEQUENCE 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indicate 1; Sequence=Displayed;
-1-TISSUB SPECIFICITY: Plasma FN (soluble dimeric form) is secreted by hepatocytes. Cellular FN (dimeric or cross-linked multimeric forms), made by fibrolasts, epithelial and other cell types, is deposited as fibrils in the extracellular matrix.
-1- PTM: Sulfaced (By similarity).
-1- SIMILARITY: Contains 12 fibronectin type I domains.
-1- SIMILARITY: Contains 15 fibronectin type III domains.
-1- SIMILARITY: Contains 15 fibronectin type III domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           PARTIAL SEQUENCE.
MEDLINE-83117805; PubMed-6218503;
Petersen T.E., Thorgersen H.C., Skorstengaard K., Vibe-Pedersen K.,
Salt P., Sottrup-Jensens L., Magnusson S.;
"Partial primary structure of bovine plasma fibronectin: three types
                                                                                                                                                                                                                                                                                                                                                                               Korstengaard K., Jensen M.S., Sahl P., Petersen T.E., Magnusson S.,
'Complete primary structure of bovine plasma fibronectin.",
our. J. Biochem. 161:441-453 (1986).
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some forms
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MEDLINE-83221567; PubMed-6304699;
Kornblihtt A.R., Vibe-Pedersen K., Baralle F.E.;
"Isolation and characterization of cDNA clones for human and bovine
                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
                      33 QAQQIVQPPSPVAVSQSKPGCFDNGKHYQINQQWERTYLGNALVCTCYG
   1 QAQQMVQPQSPVAVSQSKPGCYDNGKHYQINQQWERTYLGNVLVCTCYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Event=Alternative splicing; Named isoforms=1; Comment=A number of isoforms are produced. Each of domain" and the connecting strand 3 are present in fibronectin and absent in others;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of internal homology.";
Proc. Natl. Acad. Sci. U.S.A. 80:137-141(1983)
                                                                                                                                                                         Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                  SEQUENCE.
MEDLINE=87054047; PubMed=3780752;
                                                                                                                                                        Created)
                                                                                                                       STANDARD;
                                                                                                                                                      (Rel. 07, (Rel. 28, 1)
                                                                                                                                                                                                                                               Bos taurus (Bovine)
                                                                                                                                                                                                              Fibronectin (FN).
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                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9913;
                                                                                                                                                      01-FEB-1988 (
01-FEB-1994 (
05-JUL-2004 (
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P07589;
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Fibronectin type-III 14.
Fibronectin type-III 15.
Connecting strand 3 (CS-3) (N
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Fibronectin type-1 10.
Fibronectin type-1 11.
Cell attachment site.
By similarity.
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Fibronectin type-III 4.
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Fibronectin type-III 6.
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Fibronectin type-III 11.
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Fibronectin type-1 3.
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EMBL; K00800; AAA30521.2; -.

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Conservative

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WE SOURCE FROM N.A.

WE SEQUENCE FROM N.A.

WEDLINE-92111942; PubMed=1730390;

MEDLINE-92111942; PubMed=1730390;

MEDLINE-92111942; PubMed=1730390;

RE Gentification and characterization of alternatively spliced

RT flacentin mRNAs expressed in early Xenopus embryos.";

RL Dev. Biol. 149:357-369(1992).

CC -!- FUNCTION: Fibronectins bind cell surfaces and various compounds

CC including collagen, fibrin, heparin, DNA, and actin. Fibronectins

RC are involved in cell adhesion, cell motility, opsonization, wound

CC --- SUBMIT: Dimers or multimers of alternatively spliced variants,

CC --- SUBMIT: Dimers or multimers of alternatively spliced variants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              similarity).
ALTERNATIVE PRODUCTS:
Event-Alternative splicing; Named isoforms=1;
Comment=A number of isoforms are produced. Each of the "extra domain" and the connecting strand 3 are present in some forms of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                          QAQQMVQPQSPVAVSQSKPGCYDNGKHYQINQQWERTYLGNVLVCTCYG 49
                                                                                                                                                                                                                                                                                   MW; C2D21D486F498D5C CRC64;
                                                                                                                                                Interchain (with C-2250).
Interchain (with C-2260).
Sulfotyrosine (Potential).
Sulfotyrosine (Potential).
N-linked (GLONAC...).
O-linked (GLONAC...).
O-linked (GLONAC...).
Plinked (GLONAC...).
O-linked (GLONAC...).
Plinked (GLONAC...).
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Pred. No. 1.2e-22;
3; Mismatches 2;
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01-NOV-1997 (Rel. 35, Last sequence update)
02-UUL-2004 (Rel. 44, Last annotation update)
Fibronectin precursor.
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89.8%;
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NCBI_TaxID=8355;
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                                                                                                                                                                                                                  Pyrrolidone carboxylic acid.
Fibrin- and heparin-binding 1.
Collagen-binding.
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Heparin-binding
   HSSP; PO8353; IKBO.

HSSP; PO8353; IKBO.

InterPro; IPR006209; EGF_like.

InterPro; IPR001895; Fibrnctni.

InterPro; IPR001895; FN_III.

Pfam; PF00019; fn1; 12.

Pfam; PF00019; fn1; 12.

Pfam; PF00011; FNIYPEI.

PRINTS; PR0011; FNIYPEII.

PROSITE; PR0012; FNIYPEII.

PROSITE; PS0012; FNIYPEII.

PROSITE; PS0125; FIREOMECTINI; IPROSITE; PS01253; FIREOMECTINI; INTERPROPECTINI; IPROSITE; PS01853; FNIN; IS.
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Gaps

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By similarity.

Interchain (with C-2463) (By similarity) truterchain (with C-2459) (By similarity) N-linked (GlCNAc. . .) (Potential).

N-linked (GlCNAc. . .) (Potential).
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    type-III 16.
strand 3 (CS-3) (V region).
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
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Pred. No. 5.5e-15;
3; Mismatches 9; Indels
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Fibronectin type-II 10.
Fibronectin type-II 11.
Fibronectin type-II 11.
Fibronectin type-II 11.
Fibronectin type-II 12.
Cell attachment site.
By similarity.
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Local Similarity 71.4%;
les 35; Conservative
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                                   Inside_091740-1; Sequence=Displayed;
-!- TISSUE SPECIFICITY: In early Xenopus embryo, cellular forms of fibronectin predominate which include both extra domains. In fibronectin of embryonic and adult liver the connecting strand can be either completely excluded or included.
-!- SIMILARITY: Contains 12 fibronectin type I domains.
-!- SIMILARITY: Contains 2 fibronectin type III domains.
-!- SIMILARITY: Contains 17 fibronectin type III domains.
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Heparin-binding; Plasma; Repeat; Signal.
SIGNAL 1 31 Potential.
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Collagen-binding.
By similarity.
Cell-attachment.
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Fibronectin type I 2.
Fibronectin type I 3.
Fibronectin type I 5.
Fibronectin type I 6.
Fibronectin type I 6.
Fibronectin type I 7.
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InterPro; 1PR000083; Fibrnctn1.
InterPro; 1PR000083; Fibrnctn1.
InterPro; 1PR000895; FN III-like.
InterPro; 1PR0008562; FN III-like.
InterPro; 1PR0008562; FN TYPE_II.
Pfam; PF000041; fn1; 12.
Pfam; PF000041; fn2; 17.
PRINTS; PR00013; FNTYPEII.
SMART; SM00059; FNI TYPE_II.
SMART; SM00059; FNI TYPE_II.
SMART; SM00069; FNI; 12.
SMART; SM00069; FNI; 12.
SMART; SM00060; FNI; 17.
PROSITE; PS00022; EGF_I; 2.
PROSITE; PS01253; FIBROMECTIN_I; 11.
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Klausher R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenco, L., Marusina K.P., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E., Rownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.A., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Richards S.A., McEwan P.J., McKernan K.J., Lu X., Glubs R.A., Halton D.K., Maruy D.M., Sodergren B.J., Lu X., Glubs R.A., Avillalon D.K., Maruy D.M., Sodergren B.J., Lu X., Glubs R.A., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Alakesley R.W., Touchman J.W., Green B.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.;
T. "Generation and initial analysis of more than 15,000 full-length human RT and mouse cDNA sequences.",
P. T. "Gross Natl. Acad. Sci. U.S.A., 99:16899-16903(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W., Richardson P., "Genetic and genomic tools for Xenopus research: The NIH Xenopus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SMOUGS9; FN2; 2.
SMART; SMOOGS9; FN2; 1.
SMART; SMOOGS9; FN2; 1.
PROSITE; PS00022; FIREQUECTIN_1; 1.
PROSITE; PS00022; FIREQUECTIN_2; 1.
PROSITE; PS00823; FN3; 17.
PROSITE; PS0083; FN3; 17.
PROSITE; PS00878; WD_REPEATS_1; UNKNOWN 1.
PROSITE; PS00678; WD_REPEATS_1; UNKNOWN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match 70.5%; Score 194; DB 2; Length 240 Best Local Similarity 71.4%; Pred. No. 5.5e-15; Matches 35; Conservative 3; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Klein S., Strausberg R.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC072841; AAH72841.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GO; GO:0005576; C:extracellular; IEA.
InterPro; IPR006209; EGF like.
InterPro; IPR000083; Fibrnctn1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR003961; FW_III.
InterPro; IPR008957; FW_III-like.
InterPro; IPR001662; FW_Type_II.
InterPro; IPR001680; WD40.
Pfam; PP00040; fn2; 2.
Pfam; PF00040; fn2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PRO0013; FNTYPEII.
ProDom; PD000995; FN Type_II; 2.
SMART; SM00058; FN1; 12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dev. Dyn. 225:384-391(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            initiative.
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1 QAQQMVQPQSPVAVSQSKPGCYDNGKHYQINQQWERTYLGNVLVCTCYG 49 ò g

Search completed: September 30, 2005, 13:37:56 Job time : 36.4502 secs

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Patent No. 5455158
Patent No. 5455158
Sequence 12, Appli
Sequence 2, Appli
Sequence 1, Appli
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4, Appli
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                                                                                   5; Search time 6.30225 Seconds (without alignments) 580.396 Million cell updates/sec
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1 QAQOMVQPQSPVAVSQSKPG.....INQQWERTYLGNVLVCTCYG 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1,
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Sequence 1
Sequence 2
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
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/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd
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US-09-016-366A-12

US-08-551-356-2

PCT-US33-1268-2

US-08-9561-403-1

US-08-142-49B-14

US-08-142-49B-14

US-08-142-49B-14

US-08-140-12

US-08-140-12

US-08-140-12

US-08-140-12

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US-09-270-76-14-13-13

US-09-248-796A-19263

US-09-348-796A-19263

US-09-348-796A-19263

US-09-348-796-19263
                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
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US-08-283-857-1
PCT-US95-09819-1
                                                                                                                                                                                                                                                      513545 segs, 74649064 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUMMARIES
                                                                                     September 30, 2005, 08:57:15
                                                                                                                                                                                                                                                                                                                                                          Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries
                                                        OM protein - protein search, using sw model
                                                                                                                                               US-09-492-971B-15_COPY_4_52
                                                                                                                                                                                                          BLOSUM62
Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                length: 0
length: 2000000000
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Match Lengtĥ DB
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100.0
100.0
100.0
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Maximum DB seq
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28	57.5	20.9	7 % T	4	US-U8-343-76UA-2	acrienhac	z, Appil
29	57	20.7	587	~	US-08-871-266B-18	Sequence	18, App]
30	57	20.7	587	~	US-09-018-864A-18	Sequence	18, Appl
31	57	20.7	587	٣	US-08-871-267B-24	Sequence	24, App]
32	57	20.7	587	m	US-09-618-419-24	Sequence	e 24, Appl
33	57	20.7	593	4	US-09-949-016-7031	Sequence	7031, AF
34	56.5	20.5	272	~	US-08-160-524A-7	Sequence	7, Appli
35	26	20.4	44	-	US-08-340-812-6	Seguence	6, Appli
36	26	20.4	44	ч	US-08-459-064B-6	Sequence	6, Appli
37	26	20.4	44	~	US-08-460-421A-6	Sequence	6, Appli
38	26	20.4	44	Ŋ	PCT-US93-00909-6	Sequence	6, Appli
39	26	20.4	5405	m	US-08-718-388-9	Sequence	9, Appli
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41	55.5	20.2	2910	7	US-08-444-733-183	Sequence	183, App
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44	55.5	20.2	2910	N	US-08-485-910-183	Seguence	183, Apr
45	55.5	20.2	2910	'n	PCT-US95-06266-157	Seguence	157, App

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#### ALIGNMENTS

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RESULT 1

RESULT 1

RESULT 1

RESULT 1

SEQUENCE 16, Application US/08153799

Patent No. 576683

APPLICANT: Goodey, Andrew R

TITLE OF INVENTION: Polypeptides

NUMBER OF SEQUENCES: 23 POPETION

TITLE OF INVENTION: Polypeptides

NUMBER OF SEQUENCES: ADPRESS:
ADDRESSE: R Hain Swope, BOC Health Care Inc
STREET: 100 Mountain Avenue
CITY: Murray Hill

STATE: New Jersey

COUNTRY: USA
ZIP: 07974

COMPUTER: READABLE FORM:
MEDUUM TYPE: Ploppy disk
COMPUTER: READABLE FORM:
MEDUUM TYPE: Ploppy disk
COMPUTER: EACHTON BATS: APPLICATION DATE:
APPLICATION NUMBER: US 07/84795

FILING DATE: 06-WAR-1992

RICH APPLICATION NUMBER: US 07/84795

FILING DATE: 26-WAR-1992

RICH APPLICATION DATE: APPRICATION DATE: APPLICATION NUMBER: US 07/775952

FILING DATE: 28-APR-1990

PRIOR APPLICATION NUMBER: US 07/775952

FILING DATE: 28-APR-1990

PRIOR APPLICATION NUMBER: 28-GOT-1991

ATTORREY/AGENT INFORMATION:
NAWE: SWOOGE R Hain
REGISTRATION NUMBER: 28-GOT-1991

FILING DATE: 29-GOT-1991

FILING DATE: 21-GOT-1991

FILING DATE: 21-GOT-1991
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1 QAQQMVQPQSPVAVSQSKPGCYDNGKHYQINQQWERTYLGNVLVCTCYG 49
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Best Local Similarity
                                                                                                                                                         TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: GOLD, Lealie I.
APPLICANT: ROSTAGNO, Agueda A.
APPLICANT: BARON, Martin
APPLICANT: CAMPBELL, Iain D.
APPLICANT: WILLIAMS, Michael, J.
TITLE OF INVENTION: FIBRONECTIN FIBRIN-BINDING PEPTIDES, DNA
TITLE OF INVENTION: CODING THEREFOR AND USERS THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 275; DB 1; Length 2324; ilarity 100.0%; Pred. No. 5.1e-27; Conservative 0; Mismatches 0; Indels 0.
                                                                                                                                                                                                                                                                                                           QAQQMVQPQSPVAVSQSKPGCYDNGKHYQINQQWERTYLGNVLVCTCYG 49
                                                                                                                                                                                                   Length 2231;
                                                                                                                                                                                                                                                                                  1 QAQQMVQPQSPVAVSQSKPGCYDNGKHYQINQQWERTYLGNVLVCTCYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/283,857 FILING DATE: 01-AUG-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/714,134
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                 100.0%; Score 275; DB 1;
100.0%; Pred. No. 4.9e-27;
iive 0; Mismatches 0;
                                                                                                 NAME/KEY: Protein
LOCATION: 1..2231
OTHER INFORMATION: /note= "Human fibronectin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GOLD=1A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 2004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: BROWDY, ROGER L.
REGISTRATION NUMBER: 25,618
REPRERNCE/DOCKET NUMBER: GOLD
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEPHONE: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/08283857; Patent No. 5792742; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2324 amino acids
                HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                          49; Conservative
    protein
NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: si
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Best Local Similarity
Matches 49; Conserv
                                                                                                                                                                                                                      Best Local Similarity
    MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: D.C.
                                                                                                                                                           US-08-153-799-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                 RESULT 2
US-08-283-857-1
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                                                                            FEATURE:
                                                                                                                                                                                                                                          Matches
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1 QAQQMVQPQSPVAVSQSKPGCYDNGKHYQINQQWERTYLGNVLVCTCYG

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Gaps
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                                                                                              FIBRONECTIN FIBRIN-BINDING PEPTIDES, DNA CODING THEREFOR AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 2324;
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;Patent No. 5455158
;Patent No. 5455158
TITLE OF LINUENTION: FIBRIN BINDING DOMAIN POLYPEPTIDES AND SUBSENT AMOS TITLE OF INVENTION: FIBRIN BINDING DOMAIN POLYPEPTIDES AND HIGHDED OF PRODUCING SAME
NUMBER OF SEQUENCES: 20
CURRENT APPLICATION DATA:
PREDICATION NUMBER: US/08/58,241
FILING DATE: 04-MAY-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 QAQQMVQPQSPVAVSQSKPGCYDNGKHYQINQQWERTYLGNVLVCTCYG
                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/09819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 275; DB 5;
ilarity 100.0%; Pred. No. 5.1e-27;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                   STREET: 419 Seventh Street, N.W., Suite 300 CITY: Washington STATE: D.C. COUNTRY: USA ZIP: 20004 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICALLOL.
FILING DATE:
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/283,857
FILING DATE: 01-AUG-1994
ATTORNEY AGENT INFORMATION:
NAME: BROWDY, ROGER L.
REGISTRATION NUMBER: 25,618
FRERENCE/DOCKET NUMBER: GOLD=1A P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GOLD=1A PCT
                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
PCT-US95-09819-1; Sequence 1, Application PC/TUS9509819; GENERAL INFORMATION:
                                                                                                                                                                                                 BROWDY AND NEIMARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 526,397
FILING DATE: 21-MAY-1990
APPLICATION NUMBER: 345,952
FILING DATE: 28-APPL-1989
APPLICATION NUMBER: 291,951
FILING DATE: 29-DEC-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: 248633
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2324 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , MOLECULE TYPE: peptide PCT-US95-09819-1
                                                                                                                                                 NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AN
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INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 12
SEQUENCE CHARACTERISTICS:
LENGTH: 2386 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2446 amino acids
ATTORNEY/AGENT INFORMATION:
NAME: Plumer, Elizabeth
                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: ZymoGenet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                            US-09-016-366A-12
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                                                                                                                                                                                                                                                     Patent No. 5455158
; Patent No. 5455158
; GUY, RACHEL, PANCS
; GUY, RACHEL, PANCS
; TITLE OF INVENTION: FIBRIN BINDING DOWAIN POLYPEPTIDES AND
; USES AND METHODS OF PRODUCING SAME
; USES AND METHODS OF PRODUCING SAME
; USES AND METHODS OF PRODUCING SAME
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/58,241
FILING DATE: 04-MAY-1993
; RIGHOR DATE: 21-MAY-1993
; APPLICATION NUMBER: 526,397
FILING DATE: 21-MAY-1990
; FILING DATE: 28-APR-1989
; RILING DATE: 29-DEC-1989
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                                                                                                                                                          QAQQMVQPQSPVAVSQSKPGCYDNGKHYQINQQWERTYLGNVLVCTCYG 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 2327;
                                                                 Length 2327;
                                                                                                                                      1 QAQQMVQPQSPVAVSQSKPGCYDNGKHYQINQQWERTYLGNVLVCTCYG
                                                                                                   0; Indels
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Sequence 12, Application US/09016366A

Patent No. 595841

GENERAL INFORMATION:
APPLICANT: Stevens, Richard L.
APPLICANT: Stevens, Chifu,
TITLE OF INVENTION: MAST CELL PROTEASE PEPTIDE
TITLE OF INVENTION: INHIBITORS
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
STREET: 600 Atlantic Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 275; DB 6; 100.0%; Pred. No. 5.1e-27;
                                                               Query Match 100.0%; Score 275; DB 6; Best Local Similarity 100.0%; Pred. No. 5.1e-27; Matches 49; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MELLACOMPUTER: IBM Compart...

OPERATING SYSTEM: DOS
SOFTWARE: FastSEO for Windows Version 2.0
CURRENT APPLICATION DATA:
TAPLICATION NUMBER: US/09/016,366A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: January 30, 1998
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/037,090
FILING DATE: 05-FEB-1997
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: MA
COUNTRY: U.S.A.
7TP: 02210-2211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDALL
STREET: 600
SEQ ID NO:1:
; LENGTH: 2327
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5455158-1
                                5455158-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                32 QAQQMVQPQSPVAVSQSKPGCYDNGKHYQINQQWERTYLGNVLVCTCYG 80
                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 275; DB 2; Length 2386; 100.0%; Pred. No. 5.3e-27; cive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 2446;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Irani, Meher
TITLE OF INVENTION: HYBRID CROSS-LINKING PROTEINS
NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/551,356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 275; DB 2;
ilarity 100.0%; Pred. No. 5.4e-27;
Conservative 0; Mismatches 0;
NAME: Plumer, Elizabeth R.
REGISTRATION NUMBER: 36,637
REFERENCE/DOCKET NUMBER: B0801/7093
TELECOMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
TELEFAX: 617-720-2441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/349,762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: HOLLY, JULIE A
REGISTRATION NUMBER: 33-246
REFERENCE/DOCKET NUMBER: 92-26
TELEPHONE: 206-547-8080 ext 322
TELEPAX: 206-548-2329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: APPLICATION NUMBER: US/07/998,271 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: ZymoGenetics, Inc.
STREET: 4225 Roosevelt Way, N.E.
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/08551356
Patent No. 5830700
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 49; Conserv
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SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 1
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                                             LENGTH: 2386
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; Patent No. 6780594
; Patent No. 6780594
; GENERAL INFORMATION:
; APPLICANT: HE-STUMPP, HOLGER
; APPLICANT: KRAETZSCHMAR, JOERN
; APPLICANT: KRETZSCHMAR, JOERN
; APPLICANT: WINTERHAGER, ELKE
; APPLICANT: WINTERHAGER, ELKE
; APPLICANT: WINTERHAGER, ELKE
; APPLICANT: WINTERHAGER, ELKE
; APPLICANT: MINTERHAGER, ELKE
; TITLE OF INVENTION: METHOD FOR IN VITRO DIAGNOSIS OF ENDOMETRIOSIS
; TILE REFERENCE: SCH-1789
; CURRENT APPLICATION UNMER: US/09/961,403
; CURRENT FILING DATE: 2001-09-25
; NUMBER OF SEQ ID NOS: 15
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                                               32 QAQQMVQPQSPVAVSQSKPGCYDNGKHYQINQQWERTYLGNVLVCTCYG 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 2446;
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                                                                                                                                                                                                                            APPLICANT: Irani, Meher H.
TILE OF INVENTION: HYBRID CROSS-LINKING PROTEINS NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/12687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.0%; Score 275; DB 5; Best Local Similarity 100.0%; Pred. No. 5.4e-27; Matches 49; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/998,271
FILING DATE: 31-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Parker, Gary E
REGISTRATION NUMBER: 31-648
REFERENCE/DOCKET NUMBER: 92-26PC
                                                                                                                                                                                                                                                                                                                    ADDRESSEE: ZymoGenetics, Inc.
STREET: 4225 Roosevelt Way, N.E.
CITY: Seattle
CITY: WA
COUNTRY: USA
ZIP: 99105
                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-547-8080 ext 322
                                                                                                                                                                                  Sequence 2, Application PC/TUS9312687 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 206-548-222
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
FRUGTH: 2446 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US93-12687-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                               PCT-US93-12687-2
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                                                                                                                                       RESULT 8
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                                                                               Length 2386;
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40.0%; Score 110; DB 1; Length 188;
Best Local Similarity 51.7%; Pred. No. 1.2e-06;
Matches 15; Conservative 7; Mismatches 7; Indels
                                                                                                                                                                  1 QAQQMVQPQSPVAVSQSKPGCYDNGKHYQINQQWERTYLGNVLVCTCYG
                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Nakahata, Tatsutoshi
APPLICANT: Nakahata, Tatsutoshi
APPLICANT: Sudo, Tetsuo
APPLICANT: Sudo, Tetsuo
APPLICANT: Kojina, Katsuaki
TITLE OF INVENTION: Hematopoietic Stem Cell Growth Agent
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nels T. Lippert, White & Case
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 24-NOV-1994
CLASSIFICATION: 435
                                                                               Score 271; DB 4;
Pred. No. 1.8e-26;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Nels T. Lippert, White & Case STREET: 1155 Avenue of the Americas CITY: New York STATE: OWN YORK COUNTRY: U.S.A. ZIP: 10036-2787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97 CYDDGKTYHVGEQWQKEYLGAICSCTCFG 125
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US-08-836-854-12
'Sequence 12, Application US/08836854
'Patent No. 5874547
'GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Lippert, Nels T.
REGISTRATION NUMBER: 25,888
REFRENCE/DOCKET NUMBER: 11453
TELECOMMUNICATION INPORMATION:
TELEPAX: (212) -84-9-852
TELEPAX: (212) -84-913
INPORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acide
TOPOLOGY: 1:-
                                                                                   Query Match 98.5%;
Best Local Similarity 98.0%;
Matches 48; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , MOLECULE TYPE: protein US-08-142-449B-14
TYPE: PRT
ORGANISM: Homo sapiens
US-09-961-403-1
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GENERAL INFORMATION:
ADPLICANT: RUDSLAHTI, ERKKI I.
APPLICANT: RUDSLAHTI, ERKKI I.
APPLICANT: RUDSLAHTI, ERKKI I.
APPLICANT: RUDSLAHTI, ERKKI I.
APPLICANT: MORLA, ALEX
TITLE OF INVENTION: MODULATING FIBRONECTIN EXTRACELLULAR MATRIX ASSEMBLY
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: CAMPBELL AND FLORES
STREET: 4370 LA JOLLA VILLAGE DRIVE, STE 700
CITY: SAN DIEGO
STATE: CALIFORNIA
COUNTRY: UNITED STATES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 110; DB 2; Length 474;
Pred. No. 3.7e-06;
7; Mismatches 7; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/340,812
FILING DATE: 1-NOV-1994
CLASSIFICATION NUMBER: US/08/21,626
FILING APPLICATION UNDER: 08/021,626
FILING DATE: 16-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: BELLAS, CHRISTINE M.
REGISTRATION NUMBER: 34,122
REFERENCE/DOCKET NUMBER: P-LA 9442
TELECOMMUNICATION INFORMATION:
MAT FOLIATION INFORMATION:
MAT FOLIATION INFORMATION:
MAT FOLIATION INFORMATION:
MAT FOLIATION INFORMATION:
                          PatentIn Release #1.0, Version #1.30
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                                                                                                                                                  CLASSIFICATION 1435
PRIOR APPLICATION DATA;
PRIOR APPLICATION NUMBER: 317721/1994
FILING DATE: 29-NOV-1994
ATTORNEY/AGENT INFORMATION;
NAME: Browdy, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: HASHINO-1
TELECOMMUNICATION INFORMATION;
TELECOMMUNICATION INFORMATION;
TELEFAX: (202) 528-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS;
                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/836,854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 7, Application US/08340812
Patent No. 5629291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 51.7%;
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : 474 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: 619-535-9001
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TOPOLOGY: linear;
; MOLECULE TYPE: peptide
US-08-836-854-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
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                          SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-340-812-7
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APPLICANT: HASHINO, Kimikazu
APPLICANT: MATSUSHITA, Hideyuki
APPLICANT: MATSUSHITA, Hideyuki
APPLICANT: KATO, Ikunoshin
TITLE OF INVENTION: METHOD OF PRODUCTION OF TRANSFECTED CELLS
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street N.W. Ste. 300
CITY: Washington
STATE: D.C.
CONTYRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SUGFWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION DATE:
FLING DATE:
FLIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 12
US-08-836-854-9
iSequence 9, Application US/08836854
patent No. 5824547
GENERAL INFORMATION:
APPLICANT: HASHINO, Kimikazu
APPLICANT: MATUSHITA, Hideyuki
APPLICANT: MATUSHITA, Hideyuki
APPLICANT: KATO, Ikunoshin
TITLE OF INVENTION: METHOD OF PRODUCTION OF TRANSFECTED CELLS
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSE: Browdy and Neimark
ADDRESSE: Browdy and Neimark
ADDRESSE: Browdy and Neimark
ADDRESSE: Browdy and Neimark
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street N.W. Ste. 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IRM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              380 CYDDGKTYHVGEQWQKEYLGAICSCTCFG 408
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP95/02425
FILING DATE: 29-NOV-1995
PRIOR APPLICATION NUMBER: 317721/1994
APPLICATION NUMBER: 317721/1994
ATTORNEY/AGENT INPORMATION:
NAME: Browdy, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/POCKET NUMBER: 25,618
REFERENCE/POCKET NUMBER: 25,618
REFERENCE/POCKET NUMBER: 25,618
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 422 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 51.7
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-836-854-12
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Gaps

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TOPOLOGY:
                                                                                                US-08-460-421A-7
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Sequence 7, Application US/08459064B
Patent No. 574762
GENERAL INROMATION:
APPLICANT: RUOSLAHTI, ERKKI I.
APPLICANT: CANDENGES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: CAMPBELL & FLORES LLP
STREET: ALIOERSES:
COUNTRY: UNITED STATES
COUNTRY: UNITED STATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                               Query Match 29.1%; Score 80; DB 1; Length 42; Best Local Similarity 42.9%; Pred. No. 0.0017; Matches 12; Conservative 7; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29.1%; Score 80; DB 1; Length 42; 42.9%; Pred. No. 0.0017;
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                                                                                                                                                                                                                                                                                                                                                                     22 YDNGKHYQINQQWERTYLGNVLVCTCYG 49
                                                                                                                                                                                                                                                                                                                                                                                                          4 YDDGKTYHVGEQWQKEYLGAISSSTSFG 31
                                  LENGTH: 42 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         42 amino acids
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                    , MOLECULE TYPE: peptide US-08-340-812-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
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US-08-459-064B-7
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4 YDDGKTYHVGEQWQKEYLGAISSSTSFG 31

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Sequence 7, Application US/08460421A

Patent No. 5837813

GENERAL INFORMATION:

APPLICANT: RUOSLAHTI, ERKKI I.

APPLICANT: MORLA, ALEX

TITLE OF INVENTION: PIBRONECTIN BINDING SITES AND METHODS OF

TITLE OF INVENTION: MODULATING FIBRONECTIN EXTRACELLULAR MATRIX ASSEMBLY

NUMBER OF SEQUENCES: 35

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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29.1%; Score 80; DB 2; Length 42;
Best Local Similarity 42.9%; Pred. No. 0.0017;
Matches 12; Conservative 7; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

CLASSIFICATION : 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/829,462

FILING DATE: 31-JAN-1992

PRIOR APPLICATION NUMBER: US 07/829,462

FILING DATE: 31-JAN-1992

PRIOR APPLICATION NUMBER: US 08/021,626

FILING DATE: 16-FEB-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/021,626

FILING DATE: 16-FEB-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/340,812

FILING DATE: 17-NOV-1944
                                                                                                                                                                                                                                                 ADDRESSEE: CAMPBELL & FLORES LLP
STREET: 4370 LA JOLLA VILLAGE DRIVE, STE 700
CITY: SAN DIEGO
STATE: CALIFORNIA
COUNTRY: UNITED STATES
ZIP: 92122
COMPITER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Search completed: September 30, 2005, 08:58:05 Job time : 7.30225 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 08/340,812
FILING DATE: 17-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: CAMEBELL, CATHERY A.
REGISTRATION NUMBER: 31,815
REPERRNCE/POCKET NUMBER: P-LA 1542
TELECOMUNICATION INFORMATION:
TELEPHONE: 619-535-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YDDGKTYHVGEQWQKEYLGAISSSTSFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : 42 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , MOLECULE TYPE: peptide US-08-460-421A-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
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# GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

September 30, 2005, 08:57:20; Search time 37.0257 Seconds (without alignments) 549.366 Million cell updates/sec Run on:

US-09-492-971B-15\_COPY\_4\_52 Perfect score:

275 1 QAQQMVQPQSPVAVSQSKPG.....INQQWERTYLGNVLVCTCYG 49 Segmence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

1846076 segs, 415116000 residues

1846076 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

Published Applications AA:\*

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2: /cgn2\_6/ptodata/2/pubpaa/USO7\_PUBCOMB.pep:\*

4: /cgn2\_6/ptodata/2/pubpaa/USO6\_PUBCOMB.pep:\*

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12: /cgn2\_6/ptodata/2/pubpaa/USO8\_PUBCOMB.pep:\*

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10: /cgn2\_6/ptodata/2/pubpaa/USO8\_PUBCOMB.pep:\*

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16: /cgn2\_6/ptodata/2/pubpaa/USO8\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Description	Sequence 4, Appli										
ΩΙ	10 US-09-940-235-4	US-10-171-311-64	US-10-236-031B-70	US-10-374-979-98	US-10-182-936A-98	US-10-477-238A-677	US-10-680-287A-677	US-10-477-173-677	US-10-450-763-52638	US-09-925-302-548	US-09-925-302-548
DB	10	14	15	15	15	16	16	17	18	0	10
% Query e Match Length DB ID	259	2328	2328	2328	2328	2328	2328	2328	2474	231	231
% Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	98.5	98.5
Score	275	275	275	275	275	275	275	275	275	271	271
Result No.	-	7	٣	4	2	9	7	60	σ	10	11

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US-10-144-194A-52 US-10-491-566-52 US-10-741-601-354 US-10-741-601-359 US-10-741-601-359 US-10-741-601-359 US-10-741-601-359 US-10-741-601-369 US-10-741-601-369 US-10-741-601-363 US-10-741-601-364 US-10-741-601-364 US-10-741-601-366 US-10-741-601-366 US-10-741-601-366 US-10-741-601-366 US-10-741-601-366 US-10-741-601-366 US-10-741-601-366 US-10-741-601-366 US-10-741-601-366 US-10-741-601-366 US-10-741-601-366 US-10-741-601-366 US-10-741-601-366 US-10-741-601-366 US-10-741-601-366 US-10-741-601-366 US-10-741-601-366 US-10-287-436A-137 US-10-287-436A-137 US-11-940-130-28	10-741-601- 10-788-792- 10-618-281- 10-741-600- 10-868-577A 10-485-758- 10-485-758-
115 116 117 117 118 118 118 119 119 119 119 119 119 119	116 116 118 118
463 463 463 642 642 657 657 1173 1173 1173 1173 1173 1173 1173 11	2386 2386 2386 2386 2386 2386 2386
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	
	271 271 271 271 271 271 256
2 1 1 1 1 1 1 2 2 2 2 2 2 2 2 2 2 2 2 2	0 6 6 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4

### ALIGNMENTS

GENERAL INVOCATION:

APPLICANT: Sahni, Girish
APPLICANT: Sahni, Girish
APPLICANT: Sahni, Girish
APPLICANT: Ray, Chait
APPLICANT: Sundaran, Vasudha
APPLICANT: Vadav, Mahavir
APPLICANT: Yadav, Mahavir
APPLICANT: RAGACTERISTICS AND A PROCESS FOR THE PREPARATION OF SAID
TITLE OF INVENTION: PROTEIN
TITLE OF INVENTION: PROTEIN
TITLE OF INVENTION: PROTEIN
TITLE OF INVENTION: OF APPLICANTON NUMBER: US/09/940,235
CURRENT APPLICATION NUMBER: US/09/940,235
CURRENT APPLICATION NUMBER: US/09/911,349
PRIOR APPLICATION NUMBER: 1099-12-23
PRIOR APPLICATION NUMBER: IN 3825/DEL/98
PRIOR APPLICATION NUMBER: IN 3825/DEL/98
NUMBER OF SEQ ID NOS: 28
SOFTWARE: FastESEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 259
TUNDE: DEPT. Sequence 4, Application US/09940235 Publication No. US20030059921A1 GENERAL INFORMATION:

Gaps 0 Length 259; Indels 100.0%; Score 275; DB 10; 100.0%; Pred. No. 5.4e-27; ative 0; Mismatches 0; Query Match 100. Best Local Similarity 100. Matches 49; Conservative

ORGANISM: Homo sapiens

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Gaps

. 0

Indels

Length 2328;

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Query Match 100.0%; Score 275; DB 15; Best Local Similarity 100.0%; Pred. No. 6.3e-26; Matches 49; Conservative 0; Mismatches 0;
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                                                                                                                                                                    US-10-374-979-98
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                                      1 QAQQMVQPQSPVAVSQSKPGCYDNGKHYQINQQWERTYLGNVLVCTCYG 49
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Sequence 70, Application US/10236031B
GENERAL INFORMATION:
APPLICANT: Gordon, Gavin J.
APPLICANT: Gordon, Gavin J.
APPLICANT: Gullans, Steven R.
APPLICANT: Gullans, Steven R.
APPLICANT: Gullans, Steven R.
APPLICANT: Glanco, Raphael
TITLE OF INVENTION: Diagnostic and Prognostic Tests
FILE REFERENCE: B0801/7025 (JRV/JAV)
CURRENT APPLICATION UNMERS: US/10/236,031B
CURRENT FILING DATE: 2002-09-05
PRIOR PRILING DATE: 2001-09-05
PRIOR FILING DATE: 2001-09-05
PRIOR FILING DATE: 2001-09-05
NUMBER OF SEQ ID NOS: 102
SOFTWARE: PATENTIN VOWBER: US 60/407,431
NUMBER OF SEQ ID NOS: 102
SEQ ID NO 700
FENOMER.
                                                                                                                                   ; Sequence 64, Application US/10171311; Publication No. US20030087270A1; GENERAL INFORMATION:
                                                                                                                                                                                  APPLICANT: Schlegel, Robert
APPLICANT: Chen, Yan
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Zhao, Xumei
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ORGANISM: Homo sapiens
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Best Local Similarity
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TYPE: PRT
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US-10-184-9364-98

Sequence 98, Application US/10182936A

Sequence 98, Application US/10182936A

Sequence 98, Application Wo. US20040038860A1

GENERAL INFORMATION:

APPLICANT: Allan, Kristina M.

APPLICANT: Bhat, Bheem

APPLICANT: Bhat, Bheem

APPLICANT: Bradness, Veronique

APPLICANT: Pagagnes, Veronique

APPLICANT: Sandens, John

APPLICANT: Yaworsky, Paul

ITLE 0F INVENTION: Reagents and Method for Modulating DKK-Mediated Interactions

FILE REFERENCE: 032796-143

CURRENT APPLICATION NUMBER: US/10/182,936A

CURRENT APPLICATION NUMBER: US 60/291,311

PRIOR FILING DATE: 2002-06-17

PRIOR PILING DATE: 2001-05-17

PRIOR PILING DATE: 2001-05-17

PRIOR PILING DATE: 2002-03-04

NUMBER OF SEQ ID NOS: 216

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 98

LENGTH: 2328

WAVE: DET
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1 QAQQMVQPQSPVAVSQSKPGCYDNGKHYQINQQWERTYLGNVLVCTCYG 49
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                                                       5 QAQQMVQPQSPVAVSQSKPGCYDNGKHYQINQQWERTYLGNVLVCTCYG 53
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                                                                                                                                                                                               Sequence 99, Application US/10374979;
Publication No. US20030219793A1;
GENERAL INFORMATION:
APPLICANT: John P. Carulli et al.;
TITLE OF INVENTION: THE HICH BONE MASS GENE OF 11q13.3;
FILE REFERENCE: 032796-021
CURRENT FILING DATE: 2003-03-04;
PRIOR FILING DATE: 2000-04-05;
PRIOR PLICATION NUMBER: US 09/544,398
PRIOR PLICATION NUMBER: US 09/543,771
PRIOR PLICATION NUMBER: US 09/543,771
PRIOR PLICATION NUMBER: US 09/543,771
PRIOR PLICATION NUMBER: US 09/229,319
PRIOR FILING DATE: 2000-04-05
PRIOR PLICATION NUMBER: US 09/229,319
PRIOR FILING DATE: 1999-01-13
PRIOR FILING DATE: 1998-01-13
PRIOR FILING DATE: 1998-01-33
NUMBER OF SEQ ID NOS: 109
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ORGANISM: Homo sapiens
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NUMBER OF SEQ ID NOS: 812
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| GENERAL INFORMATION |
| APPLICANT: Babij, Philip |
| APPLICANT: Babij, Promit |
| APPLICANT: Babij, Promit |
| APPLICANT: Babij, Petal |
| APPLICANT: Back, Frederick J. III |
| APPLICANT: Bodine, Peter Van Nest |
| TITLE OF INVENTION: Transgenic Animal Model of Bone Mass Modulation |
| FILE REFERENCE: 2013-96-212 |
| CURRENT PAPLICATION NUMBER: US 60/290,071 |
| PRIOR FILING DATE: 2001-05-11 |
| PRIOR APPLICATION NUMBER: US 60/291,311 |
| PRIOR FILING DATE: 2001-05-17 |
| PRIOR FILING DATE: 2001-05-17 |
| PRIOR FILING DATE: 2002-02-01 |
| PRIOR FILING DATE: 2002-02-01 |
| PRIOR FILING DATE: 2002-02-01 |
| PRIOR FILING DATE: 2002-03-04 |
| NUMBER OF SEQ ID NOS: 812 |
| SOFTWARE: FastSEQ for Windows Version 4.0 |
| SEQ ID NO 677 |
| LENGTH: 2328 |
| TANDER DATE: 2018 |
| TANDER DATE: 2018 |
| SEQ ID NO 677 |
| TANDER DATE: 2018 |
| TANDER DATE: 2018
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Sequence 677, Application US/10680287A
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Babij, Philip
APPLICANT: Wavorsky, Paul
APPLICANT: Bed, Frederick J. III
APPLICANT: Bodine, Peter Van Nest
TITLE OF INVENTION Transgenic Animal Model of Bone Mass Modulation
FILE REFERENCE: 032796-179
CURRENT PILING DATE: 2003-10-08
CURRENT APPLICATION NUMBER: US/10/680,287A
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100.0%; Pred. No. 6.3e-26;
iive 0; Mismatches 0;
                                                                                                                     Query Match 100.0%; Score 275; DB 15; Best Local Similarity 100.0%; Pred. No. 6.3e-26; Matches 49; Conservative 0; Mismatches 0;
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PRIOR FILING DATE: 2002-05-13
PRIOR APPLICATION NUMBER: US 60/290,071
PRIOR PILING DATE: 2001-05-11
PRIOR APPLICATION NUMBER: US 60/291,311
PRIOR FILING DATE: 2001-05-17
PRIOR APPLICATION NUMBER: US 60/353,058
PRIOR FILING DATE: 2002-02-01
PRIOR APPLICATION NUMBER: US 60/353,058
PRIOR PRIOR APPLICATION NUMBER: US 60/351,293
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Publication No. US20040221326A1
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Matches 49; Conservative
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CORGANISM: Homo sapiens
US-10-477-238A-677
        ; ORGANISM: Homo sapiens
US-10-182-936A-98
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APPLICANT: Graham, James R.
APPLICANT: Anisowicz, Anthony
APPLICANT: Liu, Wei
TITLE OF INVENTION: HBM Variants that Modulate Bone Mass and Lipid Levels
FILE REFERENCE: 032796-135
CURRENT APPLICATION UNMBER: US/10/477,173
CURRENT FILING DATE: 2003-11-10
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                                                                                                                                                                    Length 2328;
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; Publication No. US20050196754A1
; GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 790C1P3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR FILING DATE: 2001-03-30
; PRIOR FILING DATE: 2001-03-30
; PRIOR FILING DATE: 2000-03-31
; PRIOR FLING DATE: 2000-03-31
; PRIOR PLLING DATE: 2000-03-31
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; Pred. No. 6.3e-26;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT FILING DATE: 2003-11-10

PRIOR APPLICATION NUMBER: US 60/290,071

PRIOR FILING DATE: 2001-05-11

PRIOR FILING DATE: 2001-05-11

PRIOR APPLICATION NUMBER: US 60/291,311

PRIOR FILING DATE: 2001-05-17

PRIOR FILING DATE: 2002-02-01

PRIOR FILING DATE: 2002-03-04

PRIOR FILING DATE: 2002-03-04

NUMBER OF SEQ ID NOS: 1086

SOFTWARE: FASELSEQ for Windows Version 4.0

SEQ ID NO 677
SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 677 LENGTH: 2328
                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 677, Application US/10477173; Publication No. US20050070699A1; GENERAL INFORMATION:
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1 Similarity 100.0%;
49; Conservative 0
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Best Local Similarity 100.0
                                                                            ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-680-287A-677
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Best Local Similarity
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Page

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TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
LOCATION: (44)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
LOCATION: (205)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; LOCATION: (226)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-302-548
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61 QAQQMVQPQSPVAVSQSKPGCYDNGKHYQINQQWERTYLGNALVCTCYG 109
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                                                                                        RESULT 11
US-09-925-302-548
US-09-925-302-548
Sequence 548, Application US/09925302
Publication No. US20030064072A9
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA104
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Sequence 52, Application US/10144194A

PUBLICATION NO. US20030215809A1

GENERAL INFORMATION:

APPLICANT: OriGene Technologies Inc

TITLE OF INVENTION: Regulated Breast Cancer Genes

FILE REFERENCE: 3U 103 H

CURRENT PELICATION NUMBER: US/10/144,194A

CURRENT FILING DATE: 2002-06-12

NUMBER OF SEQ ID NOS: 114

SOSTWARE: Patentin version 3.0

SEQ ID NO 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 98.5%; Score 271; DB 10; Best Local Similarity 98.0%; Pred. No. 1.6e-26; Matches 48; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 271; DB 15;
Pred. No. 3.4e-26;
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                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/925,302
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05918
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 6/124,270
PRIOR APPLICATION NUMBER: 6/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 896
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 548
LENGTH: 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98.5%;
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Best Local Similarity 98.0
Matches 48; Conservative
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                        LOCATION: (504)..(541)
OTHER INFORMATION: Type II fibronectin collagen-binding domain proteins domain
OTHER INFORMATION: identified by eMATRIX, accession number BL00023, p-value=8.920e-3
OTHER INFORMATION: raw score of 24.31
                                                                                                                                                                                                                                                                                                                      LOCATION: (701)..(2267)
OTHER INFORMATION: Fibronectin type III domain identified by PFam, accession
OTHER INFORMATION: name fn3, E-value=3.1e-275, PFam score of 927.8
PEATURE:
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; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-925-302-548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: (44)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98.5%; Score 271; DB 9; Length 231; 98.0%; Pred. No. 1.6e-26; Live 0; Mismatches 1; Indels
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: LOCATION: (1)...(2474)

: OTHER INFORMATION: Xaa = X or * as defined in Table 2

US-10-450-763-5638
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US-09-925-302-548
US-09-925-302-548
Septication US/09925302
Patent No. US20020044941A1
GENERAL INFORMATION:
PRIOR FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
SOFTWARE: CUSTOM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.0
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Best Local Similarity 98.0
Matches 48; Conservative
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LENGTH: 231
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                   ORGANISM: Homo sapiens
                                                                                                                                                                                   NAME/KEY: DOMAIN
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NAME/KEY: DOMAIN
LOCATION: (701)...
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                                                                SEQ ID NO 52638
LENGTH: 2474
                                                                                                                  TYPE: PRT
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Search completed: September 30, 2005, 09:21:21 Job time : 37.0257 secs
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Publication No. US20050026169A1

GENERAL INFORMATION:

APPLICANT: CARGILL, Michele et al.

TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: US/10/741,600

CURRENT FILING DATE: 2003-12-22

NUMBER OF SEQ ID NOS: 73997

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 1066

LENGTH: 642
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TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
FILE REPERENCE: CL001500
CURRENT APPLICATION NUMBER: US/10/741,601
CURRENT FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 26415
SOFTWARE: FASESEQ for Windows Version 4.0
SEQ ID NO 354
LENGTH: 642
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                                                                                                                                                                                                                                                                                                                                                                    98.5%; Score 271; DB 16; Length 463; 98.0%; Pred. No. 3.4e-26; ive 0; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98.5%; Score 271; DB 16; Length 642; 98.0%; Pred. No. 4.9e-26; ive 0; Mismatches 1; Indels
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Sequence 354, Application US/10741601
Publication No. US20040166519A1
GENERAL INFORMATION:
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Matches 48; Conservative
                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-491-566-52
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ORGANISM: Homo sapiens
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Best Local Similarity
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US-10-741-600-1066
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US-10-741-601-354
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                                             Score 271; DB 17; Length 642;
Pred. No. 4.9e-26;
0; Mismatches 1; Indels C
                                               Query Match
Best Local Similarity 98.0%;
Matches 48; Conservative
; ORGANISM: Homo sapiens
US-10-741-600-1066
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bos taurus canis famil

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707.807 Million cell updates/sec
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                                  September 30, 2005, 13:30:52 ; Search time 189.55 Seconds
                                                                 1 QAQQMVQPQSPVAVSQSKPG......TSVQTTSSGSGPFTDVRAAV 262
                                                                                                                                                                                                          Description
                                                                                                                                                                                                                              Q72391
Q6mzf4
    GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                          1612378 segs, 512079187 residues
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                                                       US-09-492-971B-15_COPY_4_265
                                                                                                                                                                                                                    Q7Z391
Q6MZF4
Q6NOA6
FINC_HUMAN
Q6MZUS
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FINC_RAT
Q8C6J7
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Q6GQAS
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Maximum Match 100%
Listing first 45 summaries
                        OM protein - protein search, using sw model
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Q68DP9
Q6N025
Q68DP8
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093406
06JAN2
06DD34
Q6MZM7
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1: uniprot_sprot:*
2: uniprot_trembl:*
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Match Length DB
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homo sapien
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUB=Human colon endothel primary cell culture;
Bloecker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BX538045; CAD97984.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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SEQUENCE 749 AA; 83524 MW; C8DDF97F3ED2F0DE CRC64;
                                                                                                                                                                                                                                                                                                                                                       01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein DKFZp686B18150.
Name-DKFZp686B18150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match

99.7%; Score 1495; DB 2;
Best Local Similarity 99.6%; Pred. No. 3.1e-121;
Matches 261; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                            749 AA
                                                                                                                                                                                                                                                ALIGNMENTS
FINC_NOTVI
PINC_PEBWA
PINC_PEBWA
PINC_CANFA
PINC_CHICK
Q9H3G2
PINC_CHICK
Q7TZW7
Q862C9
Q97ZW7
Q862C9
Q97ZW7
Q862C9
Q90819
Q90819
PINC_RABIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GO; GO: 0005576; C:extracellular; IEA.
InterPro; IPR006209; EGF like.
InterPro; IPR006209; EGF like.
InterPro; IPR006209; Fir Type_II.
Pfam; PF000409; fn1; 9.
ProDom; PF000409; fn2; 2.
ProDom; PF000409; FN2; 2.
ProDom; PF00058; FN1; 9.
ProSITE; PS00022; EGF I; UNKNOWN I.
PROSITE; PS00123; FIBRONECTIN 1; 9.
PROSITE; PS01253; FIBRONECTIN 2; 2.
1328
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Q8R3F3 Q7L553 Q6PJE5 Q6MZS0 Q68CX6

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homo sapien homo sapien ambystoma m

Q6pje5 Q6mzs0 Q68cx6 Q90xq2

oryctolagus brachydanio

sapien

homo

Q6n084 O02816 Q7t182

002816 Q7T1S2 Q90XQ2 Q6N084

homo sapien homo sapien

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EAEETCFDKYTGNTYRVGDTYERPKDSMIWDCTCIGAGRGRISCTIANRCHEGGQSYKIG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EAEETCFDKYTGNTYRVGDTYERPKDSMIWDCTCIGAGRGRISCTIANRCHEGGQSYKIG 151
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TESCUELE FROM N.A.

TESCUELE FROM N.A.

THE German uterus endothel primary cell culture;

The German Human cDNA Consortium;

RA Bloecker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,

Probo G., Han M., Wiemann S.,

RA Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.

REMEL, RX460669, CAR45714.1;

RO GO.000576; C.extracellular; IEA.

BRIELPTO: IPR0002086; Aldehyd.dehydrog.

RIGETPTO: IPR0000895; Fibrichl.

RIGETPTO: IPR000895; Fibrichl.

RIGETPTO: IPR000895; Fibrichl.

RIGETPTO: IPR000995; FN III-like.

BRINTS: PR00040; fn1; 12.

BR Ffam; PP00040; fn2; 12.

BR Ffam; PR00040; fn3; 15.

BR RINTS: PR00013; FNTYPEII.

BR RINTS: PR000095; FN3; 12.

BR SWART: SM00059; FN3; 13.

BR SWART: SM00059; FN3; 15.

BR SWART: SM00050; FN3; 15.

BROSITE; PS00023; FIBRONECTIN-2; 2.

BR PROSITE; PS00023; FIBRONECTIN-2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DIWRRPHETGGYMLECVCLGNGKGEWTCKP1AERCFDHAAGTSYVVGETWEKPYQGWMWV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32 QAQQMVQPQSPVAVSQSKPGCYDNGKHYQINQQMERTYLGNALVCTCYGGSRGFNCESKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DCTCLGEGSGRITCTSRNRCNDQDTRTSYRIGDTWSKKDNRGNLLQCICTGNGRGEWKCE
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                                                                                                                                                                                                                                                                          Homo sapions (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein.
SEQUENCE 2296 AA; 252761 MW; 9AB2D723CC0CED70 CRC64;
                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99.7%; Score 1495; DB 2;
99.6%; Pred. No. 9.5e-121;
iive 0; Mismatches 1;
                                                                                                                                       PRT; 2296 AA
                                                                                                                                                                        05-JUL-2004 (TrEMBLrel. 27, Created) 05-JUL-2004 (TrEMBLrel. 27, Last seq 05-JUL-2004 (TrEMBLrel. 27, Last ann Hypothetical protein DKFZp686M04163.
                  361 RHTSVQTTSSGSGPFTDVRAAV 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RHTSVQTTSSGSGPFTDVRAAV 262
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Matches 261; Conservative
                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                        Name=DKFZp686M04163;
                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                       Q6N0A6;
05-JUL-2004
  241
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RG TISSUE=Human cervix;

RG Amsorge W. Krieger S., Regiert T., Rittmueller C., Schwager B.,

RA Amsorge W., Krieger S., Regiert T., Rittmueller C., Schwager B.,

RA Amsorge W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;

RD Kingle B. BX640802; C., Edgelor I. -

BR EMBL, BX640802; CAE46800.1; -

BR EMBL, BX640802; CAE48862; -

BR EMBL, BX640802; REJIKE.

BR InterPro; IPR006503; FW III.

BR InterPro; IPR00893; FW III.

BR InterPro; IPR00895; FW III.

BR InterPro; IPR00895; FW III.

BR InterPro; IPR00895; FW III.

BR Ffam; PF00040; fin3; 4.

BR Ffam; PF00040; fin3; 4.

BR RINTS; PR000013; FNTYPEI.

BR RINTS; PR000095; FN Type_II.

BR RART; SM00069; FN Type_II.

BR ROSITE; PS00022; EGF I; UNKNOWN I.

BR PROSITE; PS0022; EGF I; UNKNOWN I.

BR PROSITE; PS0023; FIRRONECTIN I; 9.

BR PROSITE; PS0023; FIRRONECTIN I; 9.

BR PROSITE; PS0023; FIRRONECTIN I; 9.

BROSITE; PS0023; FRIRONECTIN I; 9.

BR PROSITE; PS0023; FRIRONECTIN I; 7.

BR PROSITE; PS0023; FRIRONECTIN I; 9.

BR PROSITE; PS00853; FN3; 4.

BR PROSITE; PS0023; FRIRONECTIN I; 9.

BR PROSITE; PS0023; FRIRONECTIN I; 7.

BR PROSITE; PS0023; FRIRONECTIN I; 9.
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304 DCTCLGEGSGRITCTSRNRCNDQDTRTSYRIGDTWSKKDNRGNLLQCICTGNGRGEWKCE 363
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                                                                                                                                                                                                                                 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein DKFZp686K139 (Hypothetical protein DKFZp686F719)
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Pred. No. 4.6e-121;
                                                                                                                                                                            PRT; 1103 AA.
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                                                                                                                                                                                                                                                                                                               Name=DKFZp686K139; Synonyms=DKFZp686F219;
                                                                                                                                                                                                                 05-JUL-2004 (TrEMBLrel. 27, Created)
                                    241 RHTSVQTTSSGSGPFTDVRAAV 262
                                                           364 RHTSVOTTSSGSGPFTDVRAAV 385
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                                                                                                                                                                            PRELIMINARY;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                               (Fragment).
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                                                                                                                                     RESULT 2
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Gaps

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Length 2296;

240

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SEQUENCE OF 1-49 FROM N.A. MEDLINE=87175578; PubMed=3031656; Dean D.C., Bowlus C.L., Bourgeois S.; "Cloning and analysis of the promotor region of the human fibronectin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 973-2386 FROM N.A. (ISOFORM 3).
MEDLINE=84272258; PubMed=6462919;
Kornblihtt A.R., Vibe-Pedersen K., Baralle F.E.;
"Human fibronectin: cell specific alternative mRNA splicing generates polypeptide chains differing in the number of internal repeats.";
Nucleic Acids Res. 12:5853-5868(1984).
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SEQUENCE OF 103-481 AND 2228-2386 FROM N.A. (ISOFORMS 1; 3; 8 AND 9).
TISSUE-Peripheral blood T-cell, and Umbilical vein endothelial cells;
                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 1-38 FROM N.A.
MEDLINE=87030890; PubMed=3770189; DOI=10.1016/0014-5793(86)80029-1;
Gutman A., Yamada K.M., Kornblihtt A.R.;
Human fibronectin is synthesized as a pre-propolypeptide.";
FEBS Lett. 207:145-148(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=88233940; PubMed=3375063;
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"Sequence analysis and in vivo expression show that alternative
splicing of ED-B and ED-A regions of the human fibronectin gene are
independent events.";
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                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORM 2).

MEDINE-21600194; PubMed=11737888; DOI=10.1186/bcr325;

SCHOZ S.L., SCHOZ A.M.;

"Phenotypic and genetic alterations in mammary stroma: implications
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 28-2386 FROM N.A. (ISOFORM 3).
MEDLINE-85284965; PubMed-2992339;
McDrint A.R., Umezawa K., Vibe-Pedersen K., Baralle F.E.;
"Primary structure of human fibronectin: differential splicing may generate at least 10 polypeptides from a single gene.";
EMBO J. 4:1755-1759(1985).
                                                                                                                                                               Euteleostomi;
                                                                                                                                                                                                                                                                                                                                   Ansorge W., Krieger S., Regiert T., Rittmueller C., Schwager B., Mewes H.-W., Weil B., Amid C., Osanger A., Fobo G., Han M.,
                                                       PO2751, 056609, 095610; 014312; 014325; 014326; Q86727; Q8IVI8; Q96KP7; Q96KP8; Q96KP9; Q9HB8; Q9HAP3; Q9UMK2; 21-JUL-1986 (Rel. 01, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 25-OCT-2004 (Rel. 45, Last annotation update) Pibronectin precursor (FN) (Cold-insoluble globulin) (CIG).
                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Butele
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                              Wiemann S.;
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Godfrey H.P., Ebrahim A.A.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Proc. Natl. Acad. Sci. U.S.A. 84:1876-1880(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (ISOFORM 11).
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                                                   2386 AA
                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORMS 3; 7 AND 10).
                                                                                                                                                                                                                                                                     for tumour progression.";
Breast Cancer Res. 3:373-379(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 1257-1365 FROM N.A. ("MEDLINE=88041070; PubMed=3478690;
                                                   STANDARD;
                                                                                                                                      Name=FN1; Synonyms=FN;
                                                                                                                                                   Homo sapiens (Human)
                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                         TISSUE=Cervix;
                                                 HUMAN
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SEQUENCE OF 1712-1739 FROM N.A.
MEDLINE=87026578; PubMed=3021206;
Sekiguchi K., Klos A.M., Kurachi K., Yoshitake S., Hakomori S.,
"Human liver fibronectin complementary DNAs: identification of two
different messenger RNAs possibly encoding the alpha and beta subunits
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                                                                                                                                                                                        SEQUENCE OF 1441-1548.
MEDILTRE-8225664; PubMed=7050098;
MEDILTRE-82256664; PubMed=7050098;
Pierschbacher M.D., Ruoslahti E., Sundelin J., Lind P., Peterson P.A.;
"The cell attachment domain of fibronectin. Determination of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 32-290.
MEDLINE=84032463; PubMed=6630202;
Garciar-Pardo A., Pearlstein E., Frangione B.;
"Primary structure of human plasma fibronectin. The 29,000-dalton NH2-terminal domain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 309-608, AND COLLAGEN-BINDING.
MEDLINE=87080265; PubMed=3024962;
Owens R.J., Baralle F.E.;
"Mapping the collagen-binding site of human fibronectin by expression in Escherichia coll:";
EMBO J. 5:2825-2830(1986).
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MEDILINE=8611901; PubMed=3003095;
Oldberg A., Ruoslahti E.;
"Evolution of the fibronectin gene. Exon structure of cell attachment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             β
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 1594-2386 FROM N.A. (ISOFORM 1).
MEDLINES #8280409; PubMed=292573,
MEDLINES #8280409; PubMed=292573,
MEDLINES #8280409; PubMed=292573,
"Human cellular fibronectin: comparison of the carboxyl-terminal
portion with rat identifies primary structural domains separated
hypervariable regions "1, 1985).
Hiochemistry 24:2698-2704(1985).
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MEDLINE=22126816; PubMed=12127832; DOI=10.1053/joca.2002.0792;
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MEDLINE=91190085; PubMed=2012601;
Tressel T., McCarthy J.B., Calaycay J., Lee T.D., Legesse K.,
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                                                                                                                                                                                                                                                                                                                                    primary structure.";
J. Biol. Chem. 257:9593-9597(1982)
[11]
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J. Biol. Chem. 261:2113-2116(1986)
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DCTCLGEGSGRITCTSRNRCNDQDTRTSYRIGDTWSKKDNRGNLLQCICTGNGRGEWKCE 240
DTWRRPHETGGYMLECVCLGNGKGEWTCKPIAEKCFDHAAGTSYVVGETWEKPYQGWMWV 211
                                                                                                                 DCTCLGEGSGRITCTSRNRCNDQDTRTSYRIGDTWSKKDNRGNLLQCICTGNGRGEWKCE 271
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SEQUENCE 2477 AA; 272335 MW; D358D85C6B18207C CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein DKFZp68601166.
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Pred. No. 1e-120;
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PROSITE; PS01022; BGF 1; UNKNOWN Z.
PROSITE; PS01253; FIBRONECTIN 1; 12.
PROSITE; PS00023; FIBRONECTIN 2; 2.
PROSITE; PS50853; FN3; 17.
                                                                                                                                                                              RHTSVQTTSSGSGPFTDVRAAV 262
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PRINKTS: PR00013; PRNYPEII.
ProDom; PD000995; FN TYPe_II; 2.
SMART; SM00058; FNI; 12.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PubMed=9501082; DOI=10.1093/emboj/17.6.1606; Sasaki T., Brakebusch C., Engel J., Timpl R.; "Mac-2 binding protein is a cell-adhesive protein of the extracellular matrix which self-assembles into ring-like structures and binds betal integrins, collagens and fibronectin."; EMBO J. 17:1606-1613(1998).
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                                                                                                                                                                        MEDLINE=93015879; PubMed=1400330; Balbona K., Tran H., Godyna S., Ingham K.C., Strickland D.K., Argraves W.S.; "Fibulin binds to itself and to the carboxyl-terminal heparin-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 QAQQMVQPQSPVAVSQSKPGCYDNGKHYQINQQWERTYLGNVLVCTCYGGSRGFNCESKP
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MEDINE=59081153; PubMed=798369;
ROSTEAGN A., Williams M.J., Baron M., Campbell I.D., Gold L.I.;
"Further characterization of the NH2-terminal fibrin-binding site on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Campbell I.D.;
of the factor XIIIa crosslinking
fibronectin.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=93046665; PubMed=1423622; DOI=10.1016/0092-8674(92)90600-H; Main A.L., Harvey T.S., Baron M., Boyd J., Campbell I.D.; "The three-dimensional structure of the tenth type III module of fibronectin: an insight into RGD-mediated interactions."; cell 71:671-678(1992).
                           "Human plasma fibronectin. Demonstration of structural differences between the A- and B-chains in the III CS region."; Biochem. J. 274:731-738(1991).
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"Solution structure of a pair of fibronectin type I modules with
"Ibrin binding activity.";
J. Mol. Biol. 235:1302-1311 (1994).
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Williams M.J., Phan I., Harvey T.S., Rostagno A., Gold L.I.,
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MEDLINE=92162710; PubMed=1311202;
Baron M., Main A.L., Driscoll P.C., Mardon H.J., Boyd J.,
Campbell I.D.;
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99.6%; Pred. No. 9.9e-121;
live 0; Mismatches 1;
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Potts J.R., Phan I., Williams M.J.,
"High-resolution structural studies
site and the first type 1 module of
Nat. Struct. Biol. 2:946-950(1995).
                                                                                                                                                                                                                                                                                               region of fibronectin.";
J. Biol. Chem. 267:20120-20125(1992)
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STRUCTURE BY NMR OF 1447-1540.
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Best Local Similarity 99.6
Matches 261; Conservative
   Pande H.;
                                                                                                                                            FBLN1-BINDING SITE.
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EABETCFDKYTGNTYRVGDTYERPKDSMIWDCTCIGAGRGRISCTIANRCHEGGQSYKIG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DTWRRPHETGGYMLECVCLGNGKGEWTCKPIAEKCFDHAAGTSYVVGETWEKPYQGWMMV 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DCTCLGEGSGRITCTSRNRCNDQDTRTSYRIGDTWSKKDNRGNLLQCICTGNGRGEWKCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DTWRRPHETGGYMLECVCLGNGKGEWTCKPIAEKCFDHAAGTSYVVGETWEKPYQGWMWV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DCTCLGEGSGRITCTSRNRCNDQDTRTSYRIGDTWSKKDNRGNLLQCICTGNGRGEWKCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QAQQMVQPQSPVAVSQSKPGCYDNGKHYQINQQWERTYLGNVLVCTCYGGSRGFNCESKP
                                                                                                                                                                                                                                                                                                                                                               RC TISSUE=Uterus endochel;

RG The German CDNA Consortium;

RG The German CDNA Consortium;

RA Koehrer K., Beyer A., Mewes H.W., Weil B., Amid C., Osanger A.,

RA Koehrer K., Beyer A., Mewes H.W., Weil B., Amid C., Osanger A.,

RD GO, Han M., Wiemann S.;

Rubitced (AUG-2004) to the EMBL/GenBank/DDBJ databases.

BNBL; CR749316; CAH18171.1; -.

BNBL; CR749316; CAH18171.1; -.

BNBL; CR749316; CAH1817.1.1; -.

BRICEPTO; IPRO0309; FIDETILIS.

InterPro; IPRO0309; FIDITIS.

BRICEPTO; IPRO03096; FNIII subd.

InterPro; IPRO03096; FNIII-like.

InterPro; IPRO03096; FNIII-like.

BRINTS; PRO0012; FNYPPEII.

PFam; PPO0014; FNYPPEII.

PRINTS; PRO0014; FNYPPEII.

BRINTS; PRO0014; FNYPPEII.

BRINTS; PRO0014; FNYPPEII.

BRINTS; PRO001995; FNI; 12.

SWART; SMO0509; FNI; 12.

SWART; SMO0509; FNI; 12.

SWART; SMO0509; FNI; 12.

BROSITE; PSO0022; EGF I; UNKNOWN_I.

PROSITE; PSO0022; EGF I; UNKNOWN_I.

PROSITE; PSO0023; FIBRONECTIN.; 2.

BROSITE; PSO0023; FIBRONECTIN.; 2.

BROSITE; PSO0023; FIBRONECTIN.; 2.

ROSITE; PSO0023; FIBRONECTIN.; 2.

ROSITE; PSO0023; FIBRONECTIN.; 2.

RWSITE; PSO0023; FIBRONECTIN.; 2.

RWSITE; PSO0023; FIBRONECTIN.; 2.

RWSITE; PSO0023; FIBRONECTIN.; 2.

RWSITE; PROSITE; PSO0023; FIBRONECTIN.; 2.

RWSITE; PSO0023; FIBRONECTIN.; 2.

RWSITE; PROSITE; PSO0023; FIBRONECTIN.; 2.

RWSITE; PSO0023; FIBRONECTIN
                                                                                                                                                     25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Hypothetical protein DKFZp686K08164.
Name-DKFZp686K08164;
Homo saplann (Human).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99.5%; Score 1491; DB 2; 99.2%; Pred. No. 2.1e-120; rative 1; Mismatches 1;
                                                                                                                      Ź
                                                                                                                      2267
  364 RHTSVQTTSSGSGPFTDVRAAV 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RHTSVQTTSSGSGPFTDVRAAV 262
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es 260; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
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                                                                                                                    Q68DP9
Q68DP9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                             RESULT 7

0680P9

07680P9

07680P9

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07 25-0

07 25-0

08 44P0

08 6804

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         124 QAQQMVQPQSPVAVSQSKPGCYDNGKHYQINQQWERTYLGNALVCTCYGGSRGFNCESKP 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EAEETCFDKYTGNTYRVGDTYERPKDSMIWDCTCIGAGRGRISCTIANRCHEGGQSYKIG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DTWRRPHETGGYMLECVCLGNGKGEWTCKPIAEKCFDHAAGTSYVVGETWEKPYQGWMMV 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      244 DIWRRPHETGGYMLECVCLGNGKGEWTCKPIAEKCFDHAAGTSYVVGETWEKPYQGWMWV 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DCTCLGEGSGRITCTSRNRCNDQDTRTSYRIGDTWSKKDNRGNLLQCICTGNGRGEWKCE 240
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212 DCTCLGEGSGRITCTSRNRCNDQDTRTSYRIGDTWSKKDNRGNLLQCICTGNGRGEWKCE 271
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein.
SEQUENCE 2357 AA; 259090 MW; BEAE3990E27E532A CRC64;
                                                                                                                                                                                                            25-0CT-2004 (TrEMBLrel. 28, Created)
25-0CT-2004 (TrEMBLrel. 28, Last sequence update)
25-0CT-2004 (TrEMBLrel. 28, Last annotation update)
Hypothetical protein DKFZp686F10164.
Name-DKFZp686F10164;
                                                                                                                                                                             PRT; 2357 AA
                                    RHTSVQTTSSGSGPFTDVRAAV 262
                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
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Gaps

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PRELIMINARY;
                                                                                                                         NCBI_TaxID=9606;
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                                                                                                                                                                                             RC TISSUE=Human modmetrium carcinoma cell line;

TISSUE=Human modmetrium carcinoma cell line;

TISSUE=Human modmetrium;

TISSUE=Human modmetrium;

A Ablert R., Moosmayer P., Schupp I., Wellenreuther R.,

RA Ablert R., Moosmayer P., Schupp I., Wellenreuther R.,

RA Ablert R., Moosmayer P., Schupp I., Wellenreuther R.,

RA Ablert R., Moosmayer P., Schupp I., Wellenreuther R.,

RA Submitted (AdG-2003) to the EmBL/GenBank/DDBJ databases.

B Moos H. W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;

ROS (50) 10005576; C:extracellular; IEA.

B ROSITE; PRO00039; FROM TILL.

B RIGERPRO; IPRO0059; FROM TILL.

B RIGERPRO; IPRO0059; FNOM TILL.

B RIGERPRO; IPRO0059; FNOM TILL.

B RIGERPRO; IPRO0059; FNOM TILL.

B REMRY; SMO0059; FNI; 12.

B RART; SMO0059; FNI; 12.

B RART; SMO0059; FNI; 12.

B ROSITE; PS00023; FRIRONECTIN 1; 12.

B ROSITE; PS00023; FIBRONECTIN 1; 12.

B ROSITE; PS00023; FIBRONECTIN 2; 2.

B RROSITE; PS00023; FIBRONECTIN 2; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 BAEETCFDKYTGNTYRVGDTYERPKDSMIWDCTCIGAGRGRISCTIANRCHEGGGSYKIG 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 BAEETCFDKYTGNTYRVGDTYERPKDSMIWDCTCIGAGRGRISCTIANRCHEGGQSYKIG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 2444;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2444 AA; 268676 MW; 71C5E8C56A84C7BC CRC64;
                                                           05-JUL_2004 (TrEMBLrel. 27, Created)
05-JUL_2004 (TrEMBLrel. 27, Last sequence update)
05-JUL_2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein DKFZp686M2451 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 1491; DB 2;
Pred. No. 2.3e-120;
0; Mismatches 2;
                                    2444 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RHTSVQTTSSGSGPFTDVRAAV 262
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Best Local Similarity 99.2
Matches 260; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein.
                                                                                                                         Homo sapiens (Human)
                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                             NCBI_TaxID=9606;
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           RESULT 8
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RESULT Q68DP8

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RA The German CDA Consortlund.

RA Mewes H.W., Weil B., Amid C., Osanger A., Pobo G., Han M., Wiemann S.;

RE Submitted (Adv-2004) to the EMBL/GenBank/DDBJ databases.

REL; GY49317; CAH18172.1; -

REL; CR749317; CAH18172.1; -

REL; PR000296; RGF like.

RINEEPPO; IPR003962; FN III sund.

RINEEPPO; IPR003962; FN III sund.

RINEEPPO; IPR003962; FN III sund.

RINEEPPO; IPR003962; FN III like.

RINEEPPO; IPR003962; FN III like.

RELMTS; PR00013; FNTYPEII.

RELMTS; PR00013; FNTYPEII.

RELNTS; PR00013; FNTYPEII.

RELNTS; RR000595; FN TYPE-II; 2.

REMRT; SM000595; FN TYPE-II; 3.

REMRT; SM000595; FN TYPE-II; 3
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                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 6.2e-119;
0; Mismatches 3;
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        Created)
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25-OCT-2004 (TrEMBLrel. 28, Last se
25-OCT-2004 (TrEMBLrel. 28, Last al
Hypothetical protein DKFZp686H0342.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98.3%; Scor
98.9%; Pred
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ID FINC BOVIN STANDARD;
AZ 077589;
DT 01-APR-1988 (Rel. 07, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Amygdala;
The German cDNA Consortium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 98.9
Matches 259; Conservative
                                                                                                                                                                                                                        Homo sapiens (Human).
                                                                                                                                                                            Name=DKFZp686H0342;
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PRINTS, PRO0012; FNTYPEI.
PRINTS, PRO0013; FNTYPEII.
PRINTS, PRO0014; FNTYPEII.
PROSTES, PRO1029; EGF 1; 2.
PROSTE; PS01023; FR Type II; 2.
PROSTE; PS01023; FIRRONECTIN 1; 12.
PROSTE; PS0023; FIRRONECTIN 2; 2.
PROSTE; PS0023; FN3, 15.
ACUTE phase; Alternative splicing; Cell adhesion; Cell shape;
                                                                                                                                              Fibronectin type-III 14.
Connecting strand 3 (CS-3) (V
Fibronectin type-III 15.
Fibronectin type-I 10.
Fibronectin type-I 11.
Fibronectin type-I 11.
                                                                                                                                                                                                                                                                                                  Cell attachment site
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Heparin-binding 2
Fibrin-binding 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Proc. Natl. Acad. Sci. U.S.A. 80:3218-3222(1983).

-!- FUNCTION: Fibronectins bind cell surfaces and various compounds including collagen, fibrin, heparin, DNA, and actin. Fibronectins are involved in cell adhesion, cell motility, opsonization, wound cell surfaces and maintenance of cell shape.

-!- SUBGNIT: Mostly heterodimers or multimers of alternatively spliced variants, connected by 2 disulfide bonds near the carboxyl ends; coll subsers extend homodimers.

-!- SUBCELLULAR LOCATION: Screted; extracellular matrix.

-!- ALTERNATIVE PRODUCTS:

Comment=A number of isoforms are produced. Each of the "extra domain" and the connecting strand 3 are present in some forms of fibronectin and absent in others;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE SPECIFICITY: Plasma FN (soluble dimeric form) is secreted by heparocytes. Cellular FN (dimeric or cross-linked multimeric forms), made by fibroblasts, epithelial and other cell types, is deposited as fibrils in the extracellular matrix.

-!- FM: Sulfaced (By similarity).
-!- SIMILARITY: Contains 12 fibronectin type II domains.
-!- SIMILARITY: Contains 15 fibronectin type III domains.
                                                                                                                                                              MEDLINE=87054047; PubMed=3780752; Skotstengaard K., Jensen M.S., Sahl P., Petersen T.E., Magnusson S.; Scomplete primary structure of bovine plasma fibronectin."; Eur. J. Biochem. 161:441-453 (1986).
                                                                                                                                                                                                                                      PARTIAL SEQUENCE.
MEDLINE-83117805; PubMed-6218503;
Petersen T.E., Thorgersen H.C., Skorstengaard K., Vibe-Pedersen K.,
Sahl P., Sottrup-Jensens L., Magnusson S.;
"Partial primary structure of bovine plasma fibronectin: three types
                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 2170-2265 FROM N.A.
MEDLINE=83221567; PubMed=6304699;
Kornblihtt A.R., Vibe-Pedersen K., Baralle F.E.;
"Isolation and characterization of cDNA clones for human and bovine
                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
Bovinae, Bos.
                                                                                                                                                                                                                                                                                                                  of internal homology.";
Proc. Natl. Acad. Sci. U.S.A. 80:137-141(1983).
 (Rel. 28, Last sequence update) (Rel. 44, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR003961; FN III.
InterPro; IPR008957; FN III-like.
InterPro; IPR003662; FN Type II.
InterPro; IPR003662; Fn Type II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP, P08253; 1KSO.
InterPro; IPR006209; EGF_like.
InterPro; IPR000083; Fibrnctnl.
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PF00040; fn2; 2.
                                                           taurus (Bovine).
01-FEB-1994 (Rel. 05-JUL-2004 (Rel. Fibronectin (FN).
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HSSP; P08253; 1KS(
                                                                                                                  NCBI_TaxID=9913;
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                                             Name=FN1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=FVB/N-3; TISSUE=Breast tumor;

MEDLINE=22388257; Pubmed=12477932; DOI=10.1073/pnas.242603899;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshlyuki S., Carninci P., Frange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
                                                                                                                                                                                                                                                                                                              EPEETCFDKYTGNTYRVGDTYERPKDSMIWDCTCIGAGRGRISCTIANRCHEGGQSYKIG
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                                                                                                                                                                                                                                          Gaps
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                    Length 2265;
                                                      Interchain (with C-2256).
Interchain (with C-2246).
Sulfortyrosine (Potential).
Sulfotyrosine (Potential).
N-linked (GlCNAC. .).
O-linked (GalNAC. .).
                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                  C2D21D486F498D5C CRC64;
                                                                                                                                                                                                                                          . 9
                                                                                                                                                                                                                     Score 1447; DB 1;
Pred. No. 1.4e-116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FINC MOUSE STANDARD; PRT; 2477 AA. P11276; Q61567; Q61568; Q61569; Q64233; Q80U14; O1-JUL-1989 (Rel. 11, Created) 29-MAR-2004 (Rel. 43, Last sequence update) 25-OCT-2004 (Rel. 45, Last annotation update) Fibronectin precursor (FN).
                                                                                                                                                                                         Phosphoserine.
                                                                                                                                                                                                                                         6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                      RHTSVQTTSSGSGPFTDVRAAV 262
                                                                                                                                                                                                                                                                                                                                                                                                                                   MM;
                                                                                                                                                                                                                     96.5%;
                                                                                                                                                                                                                              95.4%;
                                                                                                                                                                                                  249557
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Matches 250; Conservative
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2246
2250
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1944
2263
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                                                                                       MOD_RES
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DOWN-REGULATION BY GLUCOCORTICOIDS.

MEDLINE=21600963; PubMed=11737251;
Gu Y.-C., Talles J.F., Gullberg D., Timpl R., Ekblom M.;
Gu Y.-C., Talles J.F., Gullberg D., Timpl R., Ekblom M.;
"Glucocorticoids down-regulate the extracellular matrix proteins fibronectin, fibulin-1 and fibulin-2 in bone marrow stroma.";

Eur. J. Haematol. 67:176-184(2001).
-!- FUNCTION: Fibronectins bind cell surfaces and various compounds including collagen, fibrin, heparin, DNA, and actin. Fibronectins are involved in cell adhesion, cell motility, opsonization, wound healing, and maintenance of cell shape.
-!- SUBUNI: Mostly heterodimers or multimers of alternatively spliced variants, connected by 2 disulfide bonds near the carboxyl ends; to a lesser extend homodimers. Interacts with FBLNI and LGALSJBP
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A., "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Talts J.F., Weller A., Timpl R., Ekblom M., Ekblom P.; "Regulation of mesenchymal extracellular matrix protein synthesis by transforming growth factor-beta and glucocorticoids in tumor stroma."; J. Cell Sci. 108:2153-2162 (1995).
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MEDILINE=98202578; PubMed=5533887; DOI=10.1006/jmbi.1998.1616;
Copie V., Tomita Y., Akiyama S.K., Aota S., Yamada K.M., Venable R.M.,
Pastor R.W., Tktueger S., Torchia D.A.;
"Solution structure and dynamics of linked cell attachment modules of
mouse fibronectin contraining the RGD and synergy regions: comparison
with the human fibronectin crystal structure.";
J. Mol. Biol. 277:663-682(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Polly P., Nicholson R.C.; "Sequence of the mouse fibronectin-encoding gene promoter region.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=94131313; PubMed=8299972; DOI=10.1016/0378-1119(93)90036-3;
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MEDLINE-88124987; PubMed-3124113;
Blatti S.P., Foster D.N., Ranganthan G., Moses H.L., Getz M.J.;
Induction of fibronectin gene transcription and mRNA is a primary response to growth-factor stimulation of AKR-2B cells.";
Proc. Natl. Acad. Sci. U.S.A. 85:1119-1123(1988).
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Comment=A number of isoforms are produced. Each of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (By similarity).
SUBCELLULAR LOCATION: Secreted, extracellular matrix.
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gorski G., Aros M., Norton P.;
Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                      cDNA sequences.
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EABETCFDKYTGNTYRVGDTYERPKDSMIWDCTCIGAGRGRISCTIANRCHEGGQSYKIG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DTWRRPHETGGYMLECVCLGNGKGEWTCKPIAEKCFDHAAGTSYVVGETWEKPYQGWMMV 180
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Fibronectin type-III 1.
Fibronectin type-III 2.
Fibronectin type-III 3.
Fibronectin type-III 4.
Fibronectin type-III 6.
Fibronectin type-III 6.
Fibronectin type-III 7.
Fibronectin type-III 10.
Fibronectin type-III 11.
Fibronectin type-III 15.
Fibronectin type-III 16.
Fibronectin type-III 16.
Fibronectin type-III 17.
Fibronectin type-III 17.
Fibronectin type-III 17.
Fibronectin type-III 17.
Fibronectin type-II 11.
Fibronectin type-I 11.
Fibronectin type-I 12.
Cell attachment site.
By similarity.
By similarity.
By similarity.
By similarity.
By similarity.
By similarity.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
NCBI_TaxID=10116;
                                                                                                                                                 (extra domain 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 2477;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Score 1419.5; DB 1; Length; Pred. No. 3.7e-114; 11; Mismatches 6; Indels
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13-AUG-1987 (Rel. 05, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
Fibronectin precursor (FN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RHTSVQTTSSGSGPFTDVRAAV 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        || ::|: |:||| |||| ||
RH-ALQSASAGSGSFTDVRTAI 293
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STRAIN-Fischer; TISSUE-Liver;
MEDLINE-88054951; PubMed=2445560;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 93.19
Matches 244; Conservative
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 domain" and the connecting strand 3 are present in some forms of fibronectin and absent in others,
                                                      Isoid=P11276-1; Sequence-Displayed;
TISSUB SPECIFICITY: Plasma FN (soluble dimeric form) is secreted by hepatocytes. Cellular FN (dimeric or cross-linked multimeric forms), made by fibroblasts, epithelial and other cell types, is deposited as fibrils in the extracellular matrix.

INDUCTION: Glucocorticoids suppressed mRNA expression and protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3D-structure; Acute phase; Alternative splicing; Cell adhesion; Glycoprotein; Heparin-binding; Phosphorylation; Plasma; Repeat; Signal; Sulfation.

Signal By similarity.
                                                                                                                                                                                 -!- PTM: Sulfated (By similarity).
-!- SIMILARITY: Contains 12 fibronectin type I domains.
-!- SIMILARITY: Contains 2 fibronectin type II domains.
-!- SIMILARITY: Contains 17 fibronectin type III domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fibronectin.
Fibrin- and heparin-binding
Collagen-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           junction assembly; IDA. IMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fibronectin type-1 1.
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Fibronectin type-1 3.
Fibronectin type-1 4.
Fibronectin type-1 6.
Fibronectin type-1 6.
Fibronectin type-11 7.
Fibronectin type-11 7.
Fibronectin type-11 7.
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Heparin-binding 2
Fibrin-binding 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; 197006209; EGF like.
InterPro; 19R006083; Fibracia.
InterPro; 19R000083; Fibracia.
InterPro; 19R000962; Fibracia.
InterPro; 19R000957; FNIII subd.
InterPro; 19R000957; FN III.
InterPro; 19R000957; FN III.like.
InterPro; 19R000957; FN Type II.
Pfam; PF00040; fn2; 2.
Pfam; PF00041; fn3; 17.
PROSTIE; PR00014; FN Type II; 2.
PROSTIE; PS00025; EN Type II; 2.
PROSTIE; PS00023; FIBRONECTIN 1; 12.
PROSTIE; PS00023; FIBRONECTIN 1; 12.
PROSTIE; PS00023; FIBRONECTIN 2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GO; GO:0007155; P:cell adhesion; IDA.
GO; GO:0007044; P:cell-substrate junc
GO; GO:0042060; P:wound healing; IMP.
                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL, BC051082, AAH51082.1; --
EMBL, Z22729; CAA80422.1; --
EMBL, X82402; CAA57796.1; --
EMBL, X93167; CAA57796.1; --
EMBL, M18194; AAA37656.1; --
EMBL, S45680; AAA37636.1; --
PIR, 148349; 148349.
PIR, 148349; 148349.
PDB; ZMFN; NWR; @=1446-1630.
PDB; ZMFN; NWR; @=1446-1630.
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1; Gaps

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Fibronectin type-III 11.
Fibronectin type-III 12.
Fibronectin type-III 13 (extra domain 2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DR InterPro; IPR006209; EGF like.

DR InterPro; IPR003962; FINIT subd.

InterPro; IPR003962; FNIII subd.

DR InterPro; IPR003962; FNIII subd.

DR InterPro; IPR003962; FNIII subd.

InterPro; IPR004962; FN III.

DR Fdm; PF00039; Fn1; 12.

DR Pfam; PF00041; Fn2; 2.

DR PRINTS; PR00013; FNTYPEII.

DR PRINTS; PR00013; FNTYPEII.

DR PROSTIE; PS00022; EGF 1; 2.

PROSITE; PS00022; EGF 1; 2.

PROSITE; PS00023; FIBROMECTIN 1; 12.

PROSITE; PS00023; FIBROMECTIN 2; 2.

PROSITE; PS00023; FIBROMECTIN 3; 17.

PROSITE; PS00023; FIBROMECTIN 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fibrin- and heparin-binding 1. Collagen-binding.
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Fibronectin type-I 8.
Fibronectin type-I 9.
Fibronectin type-III 2
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Fibronectin type-III
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Fibronectin type-III
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Fibrin-binding 2
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    "" "Instruction and characterization of fibronectin-alpha 1-microglobulin complex in rat plasma.";

"Complex in rat plasma.";

"Electronection in the complex in rat plasma.";

"Electronectins bind cell surfaces and various compounds including collagen, fibrin, heparin, DNA, and actin. Fibronectins are involved in cell adhesion, cell motility, opsonization, wound healing, and maintenance of cell shape.

"SUBUNIT: Mostly heterodimers of alternatively spliced variants, connected by 2 disulfide bonds near the carboxyl ends, to a lesser extend homodimers. Interacts with FBLNI, AMBP and LGALSJBP (By similarity).

"SUBCELLULAR LOCATION: Secreted; extracellular matrix."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Odermatt E., Tamkun J.W., Hymes R.O.;
"Repeating modular structure of the fibronectin gene: relationship to
protein structure and subunit variation.";
proc. Natl. Acad. Sci. U.S.A. 82:6571-6575(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name-4; Synonyms-Landa-RLE6;

1801d=P04937-4; Sequence-VSP 003260;

1801d=P04937-4; Sequence-VSP 003260;

1801d=P04937-4; Sequence-VSP 003260;

1801d=P04937-4; Sequence-VSP 003260;

by hepatocytes. Cellular FN (dimeric or cross-linked multimeric forms), made by fibrioblasts, epithelial and other cell types, is deposited as fibrils in the extracellular matrix.

1- PTM: Sulfated (By similarity).

1- SIMILARITY: Contains 12 fibronectin type I domains.

1- SIMILARITY: Contains 2 fibronectin type II domains.

1- SIMILARITY: Contains 17 fibronectin type III domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 1183-1192; 1385-1399 AND 2287-2300, AND INTERACTION WITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Event=Alternative splicing, Named isoforms=4;
Comment=Each of the "extra domain" and the connecting strand 3
are present in some forms of fibronectin and absent in others;
                                                                                                                                                                                                                                                                                                        MEDINE=84082067; PubMed=6317187; DOI=10.1016/0092-8674(83)90175-7; Schwarzbauer J.E., Tamkun J.W., Lemischka I.R., Hynes R.O.; Tamkun J.W., Lemischka I.R., Hynes R.O.; "Three different fibronectin mRNAs arise by alternative splicing whithin the coding region."; Cell 35:421-431(1983).
    Scwarzbauer J.E., Patel R.S., Fonda D., Hynes R.O.;
"Multiple sites of alternative splicing of the rat fibronectin gene
                                                                                                                                                                                 Patel R.S., Odermatt E., Schwarzbauer J.E., Hynes R.O.; "Organization of the fibronectin gene provides evidence for exon shuffling during evolution."; BMBC J. 6:2565-2572(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tamkun J.W., Schwarzbauer J.E., Hynes R.O.;
"A single rat fibronectin gene generates three different mRNAs alternative splicing of a complex exon.";
Proc. Natl. Acad. Sci. U.S.A. 81:5140-5144(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 2052-2237 FROM N.A., AND ALTERNATIVE SPLICING PubMed=6089177;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PubMed=7519849;
Falkenberg C., Enghild J.J., Thogersen I.B., Salvesen G.,
Akerstrom B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 1722-1810 FROM N.A., AND ALTERNATIVE SPLICING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name=2; Synonyms=FNIÎI-13-less;
IsoId=P04937-2; Sequence=VSP_003258;
Name=3; Synonyms=Lambda-RLF4-5;
IsoId=P04937-3; Sequence=VSP_003259;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IsoId=P04937-1; Sequence=Displayed;
                                                                                                               SEQUENCE OF 1-139 AND 2382-2477 FROM N.A.
STRAIN=Fischer; TISSUE=Liver;
MEDLINE=88054950; PubMed=3119323;
                                                                                                                                                                                                                                                                                                 SEQUENCE OF 1586-2477 FROM N.A.
                                                                   ЕМВО J. 6:25/3-2580(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PubMed=3863113;
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Carraine-Coffil/Gi, TISSUE-Ovary;
Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
Adachi J., Aizawa K., Akimura T., Hara A., Hashizume W.,
Pukuda S., Furuno M., Hanaqaki T., Hara A., Hashizume W.,
Hayashida K., Hayatau W., Hirancok T., Hirackan T.,
Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
Aktoh H., Kawai J., Kojima Y., Konno H., Konno H., Konno M., Koya S.,
Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., Koya S.,
Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
A sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagawi M.,
Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.

HSSP, O96KP7, IFBR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=C57BL/6J; TISSUE=Ovary;

STRAIN=C57BL/6J; TISSUE=Ovary;

A Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., A Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watchiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Aokazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;

RIKEN integrated sequence analysis (RISA) system-384-format genome Res. 10:1757-1771(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRANIE-GYBL/GJ; IISSUE=Ovary;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAINS-C57BL/6J; TISSUE-Ovary;
STRAINS-C57BL/6J; TISSUE-Ovary;
STRAINS-20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
Franci J., Shibata K., Itoh M.,
Franci J., Shibata K.,
Franci J
                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=C57BL/60; IISSUE=Cvary;
MEDLINE=99279273; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
  length enriched library, clone:E330027I09 product:fibronectin 1, full
                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Ovary;
STRAIN=21085660; PubMed=11217851; DOI=10.1038/35055500;
RIKEN FANTOM CONSORTIUM;
"Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
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InterPro; IPR006209; EGF like.
InterPro; IPR000083; Fibrnctnl.
Pfam; PF00039; fnl; 5.
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PRINTS; PR00012; FNTYPEI
                                 insert sequence.
Mus musculus (Mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DCTCLGEGSGRITCTSRNRCNDQDTRTSYRIGDTWSKKDNRGNLLQCICTGNGRGEWKCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QAQQMVQPQSPVAVSQSKPGCYDNGKHYQINQQWERTYLGNVLVCTCYGGSRGFNCESKP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Score 1412.5; DB 1; Length 2477;
; Pred. No. 1.5e-113;
10; Mismatches 8; Indels 1;
Fibronectin type-III 14.
Fibronectin type-III 15.
Fibronectin type-III 15.
Fibronectin type-III 16.
Fibronectin type-III 17.
Fibronectin type-III 17.
Fibronectin type-I 11.
Fibronectin type-I 12.
Cell attachment site.
By similarity.
By similarity
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OBCGJ7;
O1-MAR-2003 (TrEMBLrel. 23, Created)
O1-MAR-2003 (TrEMBLrel. 23, Last sequence update)
O1-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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Best Local Similarity 92.7<sup>3</sup>
Matches 243; Conservative
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B. State and Splicing, Named isoforms=1;
Comment-A number of isoforms are produced. Each of the "extra domain" and the connecting strand 3 are present in some forms of fibronectin and absent in others;
                                                                                                                                                                                                                                                                                                                                                           DCTCLGEGNGRITCTSRNRCNDQDTRTSYRIGDTWSKKDNRGNLLQCVCTGNGRGEWKCE
                                                                      1 QAQQMVQPQSPVAVSQSKPGCYDNGKHYQINQQWERTYLGNVLVCTCYGGSRGFNCESKP
                                                                                                     EAEETCFDKYTGNTYRVGDTYERPKDSM1WDCTC1GAGRGR1SCT1ANRCHEGGQSYKIG
                                                                                                                                    DTWRRPHETGGYMLECVCLGNGKGEWTCKPIAEKCFDHAAGTSYVVGETWEKPYOGWMWV
                                                                                                                                                                  DCTCLGEGSGRITCTSRNRCNDQDTRTSYRIGDTWSKKDNRGNLLQCICTGNGRGEWKCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Isold=091740-1; Sequence=Displayed;
ISOSUE SPECIFICITY: In early Xenopus embryo, cellular forms of fibronectin predominate which include both extra domains. In fibronectin of embryonic and adult liver the connecting strand can be either completely excluded or included.

SIMILARITY: Contains 12 fibronectin type I domains.
SIMILARITY: Contains 17 fibronectin type III domains.
                                                      Gaps
                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                      3,
                                     Query Match 92.2%; Score 1382.5; DB 2; Length 296; Best Local Similarity 92.0%; Pred. No. 7e-112; Matches 240; Conservative 10; Mismatches 8; Indels 3;
       PROSITE; PS00022; EGF 1; UNKNOWN 1.
PROSITE; PS01253; FIBRONECTIN 1; 5.
SEQUENCE 296 AA; 32617 MW; A0FP5F4809FB6439 CRC64;
                                                                                                                                                                                                                                                                     01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
                                                                                                                                                                                                                                                         PRT; 2481 AA
                                                                                                                                                                                                                                                                                                              Xenopus laevis (African clawed frog).
                                                                                                                                                                                                  241 RHTSVQTTSSGS--GPFTDVR 259
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RH-ALQSASAGEALGPGTAPR 292
                                                                                                                                                                                                                                                         STANDARD;
SMART; SM00058; FN1; 5.
                                                                                                                                                                                                                                                                                               Fibronectin precursor.
                                                                                                                                                                                                                                                                                                                                       Xenopodinae, Xenopus.
                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          similarity)
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Q91740;
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FINC XENLA
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Acute phase; Alternative splicing, Cell adhesion; Glycoprotein; Heparin-binding; Plasma; Repeat; Signal. SIGNAL 1 31
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Fibronectin type-1 3.
Fibronectin type-1 4.
Fibronectin type-1 4.
Fibronectin type-1 1.
Fibronectin type-1 7.
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Fibronectin type-1 1.
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Fibrin- and heparin-binding
Collagen-binding.
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Potential
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PROSITE; PS00022; BGF 1; 2.
PROSITE; PS01253; FTBROWECTIN_1; 11.
PROSITE; PS50853; FN3; 17.
                                                                                                                                                                                                                                                                                                                                               InterPro; IPR006509; BGF_like.
InterPro; IPR00083; Fibrnctnl.
InterPro; IPR001961; FN_III.I.
InterPro; IPR008957; FN_III.I.
Fnam; PP000039; fn1; 12.
Pfam; PP00040; fn1; 12.
Pfam; PF00041; fn1; 12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR00013; FNTYPEII.
ProDom; PD000995; FN TYPE_II; 2.
SMART; SM00058; FNI; 12.
SMART; SM00059; FNI; 12.
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RC TISSUE=Embryo;

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RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Altausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschank B.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Brownstein M.S., Goares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.S., Undidin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.S., Widdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.S., Widdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein W.S., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Brownstein W.S., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Allacon E., Ketteman M., Radan A., Rodrigues S., Sanchez A.,

Rhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Richards A.C., Grimwood J., Schwutz J., Myers R.M., Butterfield Y.S.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Schein J.E.,

Jones S.J., Marra M.A.;

RA Generation and initial analysis of more than 15,000 full-length human and mouse cDNa sequences.",

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W., Richardson P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Genetic and genomic tools for Xenopus research: The NIH Xenopus initiative.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ..
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PROSITE; PS01253; FIBRONECTIN 1; 11.
PROSITE; PS00023; FIBRONECTIN 2; 1.
PROSITE; PS000678; FN3; 17.
PROSITE; PS000678; WD REPEATS 1; UNKNOWN 1.
SEQUENCE 2481 AA; 272708 WW; 4DB47E656DB8B5A3 CRC64;
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ProDom; PD000995; FN Type_II;
SMART; SM00059; FN1; 12.
SWART; SM00059; FN2; 2.
SWART; SM00060; FN3; 17.
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es 218; Conservative
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By similarity.
By sim
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
Xenopodinae, Xenopus.
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c. . .) (Potential).
c. . .) (Potential).
c. . .) (Potential).
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Last annotation update)
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83.2%; Pred. No. 1.9e-103;
ive 22; Mismatches 20;
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hes 218; Conservative
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        121 DTWRRPHETGGYMLECVCLGNGKGEWTCKPIAEKCFDHAAGTSYVVGETWEKPYQGWMWV 180

        Db
        155 DTWRRPHETGGYMLECVCLGNGKGEWTCKPVAERCYDNTAGTSYVVGQTWEKPYQGWMWV 214

        Qy
        181 DCTCLGEGGGRITCTSRNRCNDQDTRTSYRIGDTWSKKDNRGNLLQCICTGNGRGEWKCE 240

        Db
        215 DCTCLGEGNGRITCSSRNRCNDQDTRTSYRIGDTWSKTDTRGNLLQCICTGNGRGEWKCE 274

        Qy
        241 RHTSVQTTSSGRGPFTDVRAAV 262

        Db
        275 RHSSAQATGTGSNPITNIQTAL 296

        Search completed: September 30, 2005, 13:37:55

        Job time: 191.55 secs
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Human pro
Human NOV
Human pol
Human myo
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Human pol
Numan pol
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Human fib
Human fib
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Protein #
Fibronect
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                              Abo01289 Human Adn95950 Human Adm3864 Human Add39412 Human Adm38646 Human EAbr58335 NM 002 Adp59560 Human EAG5175 Proreir Add2668 Human Add39415 Human Add39415 Human Add39415 Human Add39415 Human Adr67315 Human Adr67
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100.0%; Score 1499; DB 2; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.9e-109;
Matches 262; Conservative 0; Mismatches 0; Indels 0
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AAA38647
AAA38647
ADO39112
AAA38646
AAA38646
ADG955196
ADG955196
ADG9550
ADG3960
               ADR66120
ABO01289
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Compugen Ltd.
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                  version :
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Listing first 45 summaries
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                GenCore
Copyright (c) 1993
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geneseqp1980s:*
                                                                                    OM protein - protein search, using
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50 QAQQMVQPQSPVAVSQSKPGCYDNGKHYQINQQMERTYLGNVLVCTCYGGSRGFNCESKP 109
                          110 EAEETCFDKYTGNTYRVGDTYERPKDSMIWDCTCIGAGRGRISCTIANRCHEGGQSYKIG 169
                                                                                                                                                                                                 Fibrin-binding peptide; fibronectin; fibrinolysis; fibrinogenesis; thrombus; pulmonary embolus; atherosclerosis; tumour; diagnosis; therapy.
                                                    170 DTWRRPHETGGYMLECVCLGNGKGEWTCKPIAEKCFDHAAGTSYVVGETWEKPYQGWMMV
                                                                           DCTCLGEGSGRITCTSRNRCNDQDTRTSYRIGDTWSKKDNRGNLLQCICTGNGRGEWKCE
                                            DTWRRPHETGGYMLECVCLGNGKGEWTCKPIAEKCFDHAAGTSYVVGETWEKPYQGWMWV
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/labbl = Fibrin binding domain
/note= "11 kDa Ĉ-terminal fibrin-binding domain"
2141. .2185
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                                                                                                                                                                                                                                                                                             "type 1 module 3"
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                                                                                                                                                                                                                                                                                                                 note= "type 1 module
                                                                                              241 RHTSVQTTSSGSGPFTDVRAAV 262
                                                                                                     290 RHTSVQTTSSGSGPFTDVRAAV 311
                                                                                                                                         AAR92778 standard; protein; 2324 AA
                                                                                                                                                                                                                                      cocation/Qualifiers
                                                                                                                                                                                                                                                                                                          = 4F1
                                                                                                                                                                                                                                                                                                                                                                   7F1
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/label = 1F1
                                                                                                                                                                                                                                                                                                                      200. .244
label = 5F1
                                                                                                                                                                                                                                                                                        'label = 3F1
                                                                                                                                                                                                                                                                                                 (1)
/label = (1)
/not
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/label = 7
                                                                                                                                                                  (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                              439. .467
/note= "Cy
                                                                                                                                                                                                                                                                                                                                                            439. .486
/label = 7
                                                                                                                                                                                                                                                                                  .154
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                                                                                                                                                                                     Human fibronectin.
                                                                                                                                                                                                                                                                                                                                                                               Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                           Disulfide-bond
                                                                                                                                                                                                                    Homo sapiens
Unidentified
                                                                                                                                                                  21-OCT-2004
21-JUN-1996
                                                                                                                                                      AAR92778;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DCTCLGEGSGRITCTSRNRCNDQDTRTSYRIGDTWSKKDNRGNLLQCICTGNGRGEWKCE 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DCTCLGEGSGRITCTSRNRCNDQDTRTSYRIGDTWSKKDNRGNLLQCICTGNGRGEWKCE 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   terminus (amino acids 2123-232 or 2141-2230), covering the 10F1.11F1 module pair of the protein. Fibrin-binding sites can be prepd. by enzymatic cleavage of fibronectin, peptide synthesis or by recombinant DNA techniques. They are used to detect a fibrin-binding target site, to treat disorders involving abnormal fibrinolysis or fibrinogenesis, to disrupt blodd clots and delivery of medicaments to fibrin- contgistes. They show high affinity to and slow dissociation from fibrin, and provide fast diffusion and rapid clearance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 QAQQMVQPQSPVAVSQSKPGCYDNGKHYQINQQWERTYLGNVLVCTCYGGSRGFNCESKP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human fibronectin (AAR92778) has a fibrin-binding site, close to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New fibrin-binding peptide molecules - used for the diagnosis and treatment of conditions associated with fibrin deposition, e.g. tl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 1499; DB 2; Length 2324; 100.0%; Pred. No. 6.8e-109; ive 0; Mismatches 0; Indels 0;
                                                                                                                               2171. .2183
/note= "Cys2171-Cys2183 disulfide bond"
2187. .2330
/note= "11F1
/note= "type 1 module 11"
2189. .2216
                                                                                                                                                                                                                                                                                                                                                                                       'note= "Cys2214-Cys2226 disulfide bond"
                                                                                                 /note= "Cys2144-Cys2173 disulfide bond"
                                                                                                                                                                                                                                                                                                                              /note= "Cys2189-Cys2216 disulfide bond"
/label = 10F1
/note= "type 1 module 10"
2144. .2173
                                                                                                                                                                                                                                                                                                                                                                                                                            2233. .2271
/label = 12F1
/note= "type 1 module 12"
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Matches 262; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gold LI, Rostagno AA;
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                                                                      Disulfide-bond
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The present invention relates to a method for enhancing proliferation or inducing apoptosis of erythroid progenitor cells (EPCs). The method involves culturing haematopoietic cellular populations containing EPCs in the presence of a polypeptide having an integrin very late antigen (VLA) is or VLA-4 binding site. The EPCs are useful for treating patients having induced, genetic or congenital erythroid disorders. Methods of the curvation are useful in diagnostic assays of progenitor cells, e.g. cells occurring in pathologic states such as anaemia or polycythaemia and in the study of erythroid cell development. They are used in the screening of agents which inhibit or prevent apoptosis of erythroid cells. The present sequence is a human protein related to the modulation of EPCs. This sequence is used in the invention
DCTCLGBGSGRITCTSRNRCNDQDTRTSYRIGDTWSKKDNRGNLLQCICTGNGRGEWKCE 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Modulating proliferation of erythroid progenitor cells in a hematopoietic cellular population by culturing with polypeptides containing an integrin very late antigen 5 or 4 binding site, useful in treating erythroid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 EAEETCFDKYTGNTYRVGDTYERPKDSMIWDCTCIGAGRGRISCTIANRCHEGGQSYKIG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                      Human; proliferation; apoptosis; erythroid progenitor cell; EPC; VLA; integrin very late antigen; haematopoietic cell; induced disorder; genetic disorder; congenital erythroid disorder; polycythaemia; anaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 QAQQMYQPQSPVAVSQSKPGCYDNGKHYQINQQWERTYLGNVLVCTCYGGSRGFNCESKP 60
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                                                                                                                                                                                                                                                                                                                                                                             Human protein related to modulation of proliferation of BPCs.
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100.0%; Pred. No. 6.8e-109;
ive 0; Mismatches 0;
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                                                                                                        241 RHTSVQTTSSGSGPFTDVRAAV
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Matches 262; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to obtaining a population of quiescent haematopoietic cells (HC), comprising culturing HC while adhering the cells to a polypeptide having a very late antigen-4 (VLA-4) binding site, in particular fibronectin polypeptide, so as to expand the number of HC, where the adhering provides an increased percentage of quiescent HC. Also included are inducing apoptosis of a subpopulation of HC, by contacting the cells with a polypeptide having a VLA-4 binding site under conditions to cause apoptosis of a subpopulation of HC, by contacting which enriches quiescent HC, comprising a fibronectin polypeptide. The method is useful for obtaining a cell population containing quiescent haematopoietic cells which are useful for treating a subject. Use of the VLA-4 containing peptide is useful for inducing apoptosis of a subpopulation of CD34+ HC population. The present sequence is human fibronectin which contains then VLA-4 binding site used in the method of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Obtaining hematopoietic cell population containing quiescent cells for use in treating a subject, by expanding the cells while adhered to a polypeptide containing binding sites for integrins on the cells.
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                                                                                                                                                                                                                                                                                                           antigen-4;
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                                                                                                                                                                                                                                                                                                    Human; fibronectin; VLA-4 binding site; very late an
quiescent haematopoietic cell; HC; apoptosis; CD34+.
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100.0%; Pred. No. 6.8e-109;
ive 0; Mismatches 0;
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                                                                                                               AAU74674 standard; protein; 2324 AA.
    RHTSVQTTSSGSGPFTDVRAAV 262
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                                                                                                                                                                                                                                                        Human fibronectin protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bradford
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Best Local Similarity
Matches 262; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2324 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                        WO200187071-A1
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                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Williams DA,
                                                                                                                                                                                                          09-APR-2002
                                                                                                                                                           AAU74674;
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The invention describes genes (I) which are differentially regulated in prostate cancer. (I) Is useful for diagnosing a prostate cancer in a sample comprising prostate tissue, which involves determining the number of target genes which are differentially-regulated in the sample, where the number is indicative of the probability that the sample comprises prostate cancer. (I) Is useful for assessing a therapeutic or preventive in expression levels in a sample comprising prostate tissue of target genes which are differentially-regulated in prostate cancer. (I) is also useful for identifying agente that modulate a biological activity of a polypeptide differentially-regulated in prostate cancer. (I) is also useful for identifying agent that modulate a biological activity of a polypeptide differentially-regulated in prostate cancer cells, which involves contacting a polypeptide differentially-regulated concerned in prostate cancer cells, which involves contacting a polypeptide differentially regulated concerned in prostate cancer cells, which a test agent under conditions effective for the test agent to modulate a biological activity of the polypeptide, and determining whether the test agent modulates the biological activity. (I) is useful as molecular markers, as drug targets, and for detecting, proventing or treating, determining to prostate cancer. (I) and its expression conducts are used in the diagnostic test to assay for presence of cancer conducts are used in the diagnostic test to assay for presence of cancer conducts are used in the diagnostic test to assay for presence of cancer conducts are used in the diagnostic test to assay for presence of cancer conducts are used in the diagnostic test to assay for presence of cancer conducts are used in the diagnostic test to assay for presence of cancer conducts are used in the diagnostic test to assay for presence of cancer conducts are used in the diagnostic test to assay for presence of cancer conducts are used in the diagnostic encorner. (I) is useful for assessi
DCTCLGEGSGRITCTSRNRCNDQDTRTSYRIGDTWSKKDNRGNLLQCICTGNGRGEWKCE 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel genes which are differentially regulated in prostate cancer, usef for diagnosing prostate cancer in prostate tissue sample and assessing therapeutic or preventive intervention in prostate cancer patients.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     molecular marker, drug target, cancer detection, cancer diagnosis, cancer staging, cancer grading, cancer assessing, cancer monitoring.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Prostate cancer; gene expression; differential regulation;
                                                                                                                                                                                                                                                                                                                                                                                                            Protein differentially regulated in prostate cancer #89.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 378-386; 416pp; English.
                                                                                                                                                                   ABU07486 standard; protein; 2328 AA
                                                                                                                                              RHTSVQTTSSGSGPFTDVRAAV 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (ORIG-) ORIGENE TECHNOLOGIES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-APR-2001; 2001US-0281731P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-APR-2002; 2002WO-US010824
                                                                                                                                                                                                                                                                                                                                                                      28-JAN-2003 (first entry)
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N-PSDB; ABX10391.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Jay G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                ABU07486;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mass (HBM) gene, which are found on chromosome 11q13.3. The ZmaxI and HBM genes have osteopathic activities. The genes can be used in gene therapy, antisense therapy and in the production of vaccines. They can be used in the diagnosis and treatment of bone disorders including osteoporosis, the diagnosis and treatment of bone disorders including osteoporosis, agget's disease, sclerostosis, osteomalacia and fibrous dysplasia.

ABA82038 to ABA82700 and AAG68158 to AAG68193 represent sequences used in the exemplification of the present invention
Human; high bone mass; HBM gene; Zmaxl gene; chromosome 11; 11q13.3; sequence tagged site; STS; osteoporosis; osteopathic; gene therapy; antisense therapy; vaccine; bone disorder; Paget's disease; sclerostosis; osteomalacia; fibrous dysplasia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EAEETCFDKYTGNTYRVGDTYERPKDSMIWDCTCIGAGRGRISCTIANRCHEGGQSYKIG 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EAEETCFDKYTGNTYRVGDTYERPKDSMIWDCTCIGAGRGRISCTIANRCHEGGQSYKIG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 DTWRRPHETGGYMLECVCLGNGKGEWTCKPIAEKCFDHAAGTSYVVGETWEKPYQGWMWV 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes the human Zmax1 gene and the high bone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 QAQQMVQPQSPVAVSQSKPGCYDNGKHYQINQQWERTYLGNVLVCTCYGGSRGFNCESKP
                                                                                    DCTCLGEGSGRITCTSRNRCNDQDTRISYRIGDTWSKKDNRGNLLQCICTGNGRGEWKCE
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                                                             DCTCLGEGSGRITCTSRNRCNDQDTRTSYRIGDTWSKKDNRGNLLQCICTGNGRGEWKCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New high bone mass (HBM) and Zmaxl genes and proteins useful modulating bone mass for the treatment of e.g. osteoporosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 76; Page 408-413; 443pp; English.
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                                                                                                                                           241 RHISVQTISSGSGPFIDVRAAV 262
                                                                                                                                                                     241 RHTSVQTTSSGSGPFTDVRAAV 262
                                                                                                                                                                                                                                                                                       AAG68182 standard; protein; 2328 AA
                                                                                                                                                                                                                                                                                                                                                                                                              Fibronectin protein SEQ ID NO:98.
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2000US-00544398.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-JUN-2000; 2000WO-US016951.
                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
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05-APR-2000;
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of cancer, its stage of development, the nature of genetic defect, etc. The polypeptide encoded by (1) can be used as target for therapy or drug discovery. (1) can also be used for expressing the polypeptide and thus for searching specific binding partners of the polypeptide. (1) is useful in therapeutic applications to treat prostate cancer. The identification of specific genes, and groups of genes, expressed in pathways physiologically relevant to prostate cancer permits the definition of functional and disease pathways and the delineation of targets in these pathways which are useful in diagnostic, therapeutic, and clinical applications. This is the amino acid sequence of a protein differentially
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; high bone mass; HBM; LRP5; LRP6; transgenic; bone mass modulation; gene therapy; bone density modulation; bone strength; trabecular number; bone size; bone tissue connectivity; bone disease; osteoporosis; osteomalacia; rickets; Paget's disease; neoplasm of the bone.
                                                                                                                                                                                                                                                                                                                             64
                                                                                                                                                                                                                                                                                                                                                                                   QAQQMVQPQSPVAVSQSKPGCYDNGKHYQINQQMERTYLGHVLVCTCYGGSRGFNCESKP
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                                                                                                                                                                                                                             Length 2328;
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                                                                                                                                                                                                                             100.0%; Score 1499; DB 6;
100.0%; Pred. No. 6.8e-109;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RHTSVQTTSSGSGPFTDVRAAV 262
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RHTSVQTTSSGSGPFTDVRAAV
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17-WAY-2001; 2001US-0291311P.
01-FEB-2002; 2002US-0353058P.
04-WAR-2002; 2002US-0351293P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13-MAY-2002; 2002WO-US014876
                                                                                                                                                                 regulated in prostate cancer
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                                                                                                                                                                                                                                                               Conservative
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Best Local Similarity
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                                                                                                                                                                                               Sequence 2328 AA;
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04-MAR-2002;
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                                                                                                                                                                                                                                                            Matches 262;
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Composition and transfer transportation and transportation of the gene encoding Wild type HBM gene, compositing an alteration of the gene encoding LRP5 or LRP6, or expressing comprising an alteration of the gene encoding LRP5 or LRP6, or expressing to manage that is madulated by an altered gene control sequence introduced by homologous or non-homologous recombination. The transgenic animals are for the study of bone density modulation. The polymodicatides of the invention may have a use in gene therapy. The polymodicatides of the invention may have a use in gene therapy. The polymodicatides of the invention may have a use in gene therapy. The transgenic animals and contain as is modulated relative to non-transgenic animals of the same species in more than one parameter selected from bone density, bone strength, trabecular number, bone size, or bone tissue connectivity. The transgenic animals, nucleic acids and methods are useful for identifying the compositions, which may be employed for treating or preventing bone disease, or neoplasms of the bone. The transgenic animals and nucleic acids are also useful in methods for diseases in or characterised by reduced bone density or mass. The present sequence is used in the exemplification of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DTWRRPHETGGYMLECVCLGNGKGEWTCKPIAEKCPDHAAGTSYVVGETWEKPYQGWMWV 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DCTCLGEGSGRITCTSRNRCNDQDTRTSYRIGDTWSKKDNRGNLLQCICTGNGRGEWKCE 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QAQQMVQPQSPVAVSQSKPGCYDNGKHYQINQQWERTYLGNVLVCTCYGGSRGFNCESKP
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new transgenic animals (e.g. mice), useful as models for studying bondensity modulation, developing drugs for treating or preventing bone diseases (e.g. osteoporosis), or diagnosing diseases characterized by reduced bone density.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QAQQMVQPQSPVAVSQSKPGCYDNGKHYQINQQWERTYLGNVLVCTCYGGSRGFNCESKP
                                                                                                                                                            The invention relates to novel transgenic animals expressing the high bone mass (HBM) gene, expressing the corresponding wild type HBM gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 2328;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
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100.0%; Pred. No. 6.8e-109;
ive 0; Mismatches 0;
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                                                                                                                      Disclosure; Page 532-538; 603pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          therapy; vaccine.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 100.
Matches 262; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2328 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; cervical detection; gene
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The present invention describes a method (MI) for diagnosing the presence of cancer cells or non-cancer cells in a tissue sample, or determining the prognosis or non-cancer patient. MI involves providing a set of genes that are differentially expressed in cancerous or non-cancerous conditions, determining the expression levels of the set of genes and canculating a ratio of the expression levels of the differentially expressed genes. MI is useful for diagnosing the presence of cancer cells in a tissue sample, where the cancer is malignant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pleural mesothelioma (MPM), lung adenocarcinoma, squamous carcinoma, medulloblastoma, prostate cancer, breast cancer, diffuse large B-cell lymphoma, follicular lymphoma and ovariann cancer, and for determining prognosis or outcome of a cancer patient. The ratio of expression levels of differentially expressed genes is used as an indicator of cancer type, cancer class, and/or cancer prognosis, all of which are useful for determining a course of treatment of a patient. The present sequence represents a human protein which is used in an example from the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Diagnosing cancer cells in tissue sample, or determining prognosis or outcome of cancer patient, by calculating ratio of expression levels of genes that are differentially expressed in cancer and non cancer tissues.
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                                    cancer, malignant pleural mesothelioma, MPM, lung adenocarcinoma, squamous carcinoma, medulloblastoma, prostate cancer, breast cancer; diffuse large B-cell lymphoma, follicular lymphoma, ovarian cancer;
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100.0%; Pred. No. 6.8e-109;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                              Bueno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 77; Page 369-376; 396pp; English.
                                                                                                                                                                                                                                                                                                                                     (BGHM ) BRIGHAM & WOMENS HOSPITAL INC.
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                                                                                                                                                                                                                                                                                                                                                                            Gullans SR,
                                                                                                                                                                                                                                                                             05-SEP-2001; 2001US-0317389P. 30-AUG-2002; 2002US-00236031.
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 Fibronectin SEQ ID NO:70.
                                                                                                                                                                                                                                                                                                                                                                          Jensen RV,
                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-290233/28.
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                                                                                                                                                                    WO2003021229-A2.
                                                                                                                               Homo sapiens
                                                                                                                                                                                                         13-MAR-2003.
                                                                                                                                                                                                                                                                                                                                                                          Gordon GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      invention
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                                                                                                                                                                                                                                                                                                                                                                                                       ACF12828 to ACF12947 encode the human cervical cancer marker proteins (I) given in ABR92047 to ABR92164. A higher level of expression of (I) than normal indicates the presence of cervical cancer. Also described: (1) a vector (II) containing (I); (2) a host cell (III) containing (I); and (3) assessing (M1) whether a patient is afflicted with cervical cancer, comprising comparing the level of expression of a marker in a patient's sample, and the normal level of expression of the marker in a control norectival cancer sample, where a significant increase in the level of expression of the marker in the patient's sample is an indication that the patient is afflicted with control sample is an indication that the patient is afflicted with therapy and in vaccines. (I) has cytostatic activity, and can be used in gene therapy and in vaccines (I) is useful in detecting, characterising, preventing and treating human cervical cancers. (I) may also be used in various prognostic assays, pharmacogenomics and in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     240
                                                                                                                                                                                                                                                                                              New isolated nucleic acid molecule useful for detecting, characterizing, preventing and treating human cervical cancers, in various prognostic and diagnostic assays, in pharmacogenomics and in monitoring clinical trials.
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                                                                                                                                                                                      Kamatkar S;
                                                                                                                                                                                      Monahan JE,
                                                                                                                                                                                                                                                                                                                                                                        Claim 4; Page 212-217; 386pp; English
                                                                                                                                                                                    Chen Y, Zhao X, Monah
1, Glatt K, Hoersch S;
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13-JUN-2001; 2001US-0298159P.
14-NOV-2001; 2001US-0335936P.
                                  12-JUN-2002; 2002WO-US018638
                                                                                                                                               (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          monitoring clinical trials
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                                                                                                                                                                                                                                          2003-156967/15.
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                                                                                                                                                                                                       Gannavarapu M,
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19-DEC-2002
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Length 2328; Indels 180

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The present invention relates to regulating LRP5, LRP6 or HBM activity in a subject comprising administering a composition which modulates a Dkk activity. The method is useful for modulating lipid levels and/or bone mass, and is useful in treating or diagnosing abnormal lipid levels and bone mass disorders, such as osteoporosis, bond fracture, age-related loss of bone, a chondrodystrophy, drug-induced bone disorder, high bone turnover, hypercalcaemia, hyperostosis, osteogenesis, imperfecta, osteomalacia, osteomyalitis, paget's disease, osteoarchritis, and rickets. Modulators of Dkk activity are useful for as reagents in studying bone mass and lipid level modulation, in modulating whit signaling, or treating Dkk-mediated disorders. The present sequence represents a human protein sequence related to the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Regulating LRP5, LRP6 or HBM activity in a subject, useful for modulating lipid levels and/or bone mass, and for in treating bone mass disorders, e.g. osteoporosis, comprises administering a composition which modulates
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                                                                                                                                                                                                                                                                                                                                   LRPS, LRPG, HBM; Dkk activity; Osteopathic; Antiinflammatory; Antiarthritic; bone mass disorders; osteoporosis; hypercalcaemia; hyperostosis; osteogenesis; Wnt signaling.
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                                                                                                                                                                                                                                                                                               Human protein sequence related to the invention #12.
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                                          245 RHTSVQTTSSGSGPFTDVRAAV 266
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                                                                                                                                                                    ADE82522 standard; protein; 2328
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                      RHTSVQTTSSGSGPFTDVRAAV
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01-FEB-2002; 2002US-0353058P.
04-MAR-2002; 2002US-0361293P.
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                                                                                                                                                                                                                                                       (first entry)
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Dkk activity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
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                                                                                                                                                                                                                                                       29-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Allen K,
Yaworsky 1
                      241
                                                                                                                                                                                                              ADE82522;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61
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                                                                                                                           RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to High Bone Mass (HBM), LRPS (Zmax1) and LRP6 mutants, which results in a HBM-like phenotype when expressed in a cell. The HBM-like phenotype results in bone mass modulation and/or lipid level modulation. The invention is useful for diagnosing a HBM-like phenotype in a subject and for preparing a composition for modulating bone mass and/or lipid levels in a subject suffering from e.g. osteoporosis. The present sequence was used to illustrate the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EAEETCFDKYTGWTYRVGDTYERPKDSMIWDCTCICAGRGRISCTIANRCHEGGGSYKIG 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DIWRRPHETGGYMLECVCLGNGKGEWTCKPIAEKCFDHAAGTSYVVGETWEKPYQGWMMY 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DCTCLGEGSGRITCTSRNRCNDQDTRISYRIGDTWSKKDNRGNLLQCICTGNGRGEWKCE 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EAEETCFDKYTGNTYRVGDTYER PKDSMIWDCTCIGAGRGRISCTIANRCHEGGQSYKIG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DCTCLGEGSGRITCTSRNRCNDQDTRTSYRIGDTWSKKDNRGNLLQCICTGNGRGEWKCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New nucleic acid comprising a mutation in LRP5 or LRP6, useful for diagnosing a HBM-like phenotype in a subject and for preparing a composition for modulating bone mass and/or lipid levels in a subject suffering from e.g. osteoporosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Liu W;
                                                                                                                                                                                                                                                                             Bone Mass; HBM; LRP5; Zmax1; LRP6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 1499; DB 7;
100.0%; Pred. No. 6.8e-109;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Morales A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; SEQ ID NO 677; 629pp; English.
                                                                                                     ADB98726 standard; protein; 2328 AA.
                                                                                                                                                                                                                                                                                                  bone mass modulation; osteoporosis.
RHTSVQTTSSGSGPFTDVRAAV 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Graham JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENO-) GENOME THERAPEUTICS CORP.
                                                                                                                                                                                                                                                                             therapy; High
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-MAY-2001; 2001US-0290071F.
17-MAY-2001; 2001US-029131P.
01-FEB-2002; 2002US-0353058P.
04-MAR-2002; 2002US-0361293F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-MAY-2002; 2002WO-US014877.
                                                                                                                                                                                        (first entry)
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Best Local Similarity 100.0
Matches 262; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-129214/12.
                                                                                                                                                                                                                                   Human fibronectin.
                                                                                                                                                                                                                                                                                Gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P-PSDB; ADB98703
                                                                                                                                                                                                                                                                                                                                                                                     WO200292000-A2
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                                                                                                                                                                                                                                                                             Osteopathic;
                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
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245
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                    125 DTWRRPHETGGYMLECVCLGNGKGEWTCKPIAEKCFDHAAGTSYVVGETWEKPYQGWMWV 184
                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; malignant pleural mesothelioma; MPM; tumour; lung adenocarcinoma; squamous carcinoma; medulloblastoma; prostate cancer; breast cancer; diffuse large B-cell lymphoma; follicular lymphoma; ovarian cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Diagnosing the presence of cancer or non-cancer cells in tissue sample, useful for diagnosing malignant pleural mesothelioma comprises determining ratio of expression level of a set of genes expressed in
                                                                                                  DCTCLGEGSGRITCTSRNRCNDQDTRTSYRIGDTWSKKDNRGNLLQCICTGNGRGEWKCE
DTWRRPHETGGYMLECVCLGNGKGEWTCKPIAEKCFDHAAGTSYVVGETWEKPYQGWMWV
                                                                          DCTCLGEGSGRITCTSRNRCNDQDTRTSYRIGDTWSKKDNRGNLLQCICTGNGRGEWKCE
                                                                                                                                                                                                                                                                                                                                                                                                         Human malignant pleural mesothelioma (MPM) protein #31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gullans SR, Bueno R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 77; SEQ ID NO 70; 53pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (BGHM ) BRIGHAM & WOMENS HOSPITAL INC.
                                                                                                                                                       241 RHTSVQTTSSGSGPFTDVRAAV 262
                                                                                                                                                                                                                                                                                          ADJ37157 standard; protein; 2328 AA
                                                                                                                                                                           245 RHTSVQTTSSGSGPFTDVRAAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-SEP-2002; 2002US-00236031.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-SEP-2001; 2001US-0317389P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gordon GJ, Jensen RV,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2004-141744/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; ADJ37156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cancer tissues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                       22-APR-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cytostatic.
                                                                                                                                                                                                                                                                                                                                 ADJ37157;
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Sequence 2328 AA;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tryptase-6 complex inhibitory peptides - used to treat mast cell-mediated inflammatory disorders e.g. asthma.
                                                                                                                                             EABETCFDKYTGNTYRVGDTYERPKDSMIWDCTCIGAGRGRISCTIANRCHEGGQSYKIG 120
                                                                                                                                                                                124
                                                                                                                                                                                                                                                       184
                                                                                                                                                                                                                                                                                       DCTCLGEGSGRITCTSRNRCNDQDTRTSYRIGDTWSKKDNRGNLLQCICTGNGRGEWKCE 240
                                                                                                                                                                                                                                                                                                                 DCTCLGEGSGRITCTSRNRCNDQDTRTSYRIGDTWSKKDNRGNLLQCICTGNGRGEWKCE 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mast cell protease; MCP; mouse; inhibitor; peptide substrate; asthma; tryptase-6 protein; inflammatory disorder; allergic rhinitis; urticaria; anticedema; eczematous dermatitis; atopic dermatitis; anaphylaxis; hyperproliferative skin disease; peptic ulcer; hyperresponsiveness; inflammatory skin condition; fibronectin.
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                                                                                                          64
                                                                                                                                                                   EAEETCEDKYTGNTYRVGDTYERPKDSMIWDCTCIGAGRGRISCTIANRCHEGGQSYKIG
                                                                                                                                                                                                                    DTWRRPHETGGYMLECVCLGNGKGEWTCKP1AEKCFDHAAGTSYVVGETWEKPYQGWMMV
                                                                                                                                                                                                                                        DTWRRPHETGGYMLECVCLGNGKGEWTCKPIAEKCFDHAAGTSYVVGETWEKPYQGWMWV
                                                                          QAQQMVQPQSPVAVSQSKPGCYDNGKHYQINQQWERTYLGNVLVCTCYGGSRGFNCESKP
                                                                                                        QAQQMVQPQSPVAVSQSKPGCYDNGKHYQINQQWERTYLGNVLVCTCYGGSRGFNCESKP
                                       Gaps
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0
                                     Indels
Score 1499; DB 8;
Pred. No. 6.8e-109;
; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                               RHTSVQTTSSGSGPFTDVRAAV 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW63171 standard; peptide; 2386 AA
                                                                                                                                                                                                                                                                                                                                                                                               RHTSVQTTSSGSGPFTDVRAAV 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Amino acid sequence of fibronectin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (BGHM ) BRIGHAM & WOMENS HOSPITAL.
       100.0%; FL.
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   Query Match
Best Local Similarity 100.
Matches 262; Conservative
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                           Hybrid proteins have a tissue-binding domain (TBD) from 1 protein linked to a crosslinking domain from another protein. The TBD comprises: aa 2-926, 928-1338 and especially 2-1336 of the sequence given in AAR6019; the heparin-binding domain (aa 1812-1710 of AAR60021) of fibronectin; the collagen-binding domain (aa 182-103 of AAR60021) of fibronectin; or the cell-binding domain (aa 1357-190) or 1532- 1631 of AAR60020) of fibronectin in fibronectin. DNA encoding a fibronectin- fibrinogen hybrid is given in AAQ70007, and sequences for fibronectin and fibrinogen-alpha in AAQ70008 and AAQ70009, respectively. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                   DTWRRPHETGGYMLECVCLGNGKGEWTCKPIAEKCFDHAAGTSYVVGETWEKPYQGWMNV 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          240
                                                                                                                                                                                                                                                                                                                                                                               EAEETCFDKYTGNTYRVGDTYERPKDSMIWDCTCIGAGRGRISCTIANRCHEGGQSYKIG 120
                                                                                                                                                                                                                                                                                                                                                                                                                  151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human, fibronectin, glycoprotein, extracellular matrix, motif; migration, stimulation, wound healing, periodontal tissue regeneration; metastasis; tumour; invasion; angiogenesis; inflammation; connective tissue function.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 QAQQMVQPQSPVAVSQSKPGCYDNGKHYQINQQWERTYLGNVLVCTCYGGSRGFNCESKP 60
                                                                                                                                                                                                                                                                                                                                                91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   peptides which modulate cell migration have the motif IGD - and are
                                                                                                                                                                                                                                                                                                                                                                                                       EAEETCEDKYTGNTYRVGDTYERPKDSMIWDCTCIGAGRGRISCTIANRCHEGGQSYKIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DIWRRPHEIGGYMLECVCLGNGKGEWTCKPIAEKCFDHAAGTSYVVGETWEKPYQGWMVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DCTCLGEGSGRITCTSRNRCNDQDTRISYRIGDTWSKKDNRGNLLQCICTGNGRGEWKCE
                                                                                                                                                                                                                                                                                                                                  12 QAQQMVQPQSPVAVSQSKPGCYDNGKHYQINQQWERTYLGNVLVCTCYGGSRGFNCESKP
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                                                                                                                                                                                                                                         Length 2446;
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                                                                                                                                                                                                                                       Ouery Match 100.0%; Score 1499; DB 2; Best Local Similarity 100.0%; Pred. No. 7.2e-109; Matches 262; Conservative 0; Mismatches 0;
Disclosure; Page 37-48; 87pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW99595 standard; peptide; 2477
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure, Fig 5; 57pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RHTSVQTTSSGSGPFTDVRAAV
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/label= collagen-binding domain
/note="acts as tissue-binding domain of hybrid protein"
1812. .2171
/label= heparin-binding domain
/note= "acts as tissue-binding domain of hybrid protein"
                                                                                                                                                                                                            EAEETCFDKYTGNTYRVGDTYERPKDSMIWDCTCIGAGRGRISCTIANRCHEGGQSYKIG
                                                                                                                                      QAQQMVQPQSPVAVSQSKPGCYDNGKHYQINQQWERTYLGNVLVCTCYGGSRGFNCESKP
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                                                                                                                                                                                                                                                                                                                                                    DCTCLGEGSGR I TCTSRNRCNDODTRTSYRIGDTWSKKDNRGNLLOCI CTGNGRGEWKCE
                                                                                                                  1 QAQQMVQPQSPVAVSQSKPGCYDNGKHYQINQQWERTYLGNVLVCTCYGGSRGFNCESKP
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                                                 Length 2386;
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                                               ; Score 1499; DB 2
; Pred. No. 7e-109;
0; Mismatches 0
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Matches 262; Conservative
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                Sequence 2386 AA;
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23-FEB-1995
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This sequence represents the amino acid sequence of human fibronectin, a widely distributed glycoprotein present in extracellular matrices. The protein contains the motifs IGDS (AAW99593) and IGDQ (AAW99594) which can be used in peptides to stimulate cell migration for wound healing, periodontal tissue regeneration, angiogenesis, inhibition of tumour invasion and metastasis, and in relation to inflammation or connective tissue function
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Search completed: September 30, 2005, 13:34:05 Job time: 110.675 secs

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GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on: September 30, 2005, 13:30:51; Search time 40.4373 Seconds
(without alignments)
623.404 Million cell updates/sec
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Title: Perfect score.	US-09-492-971B-15_COPY_4_265
Sequence:	1 QAQQMVQPQSPVAVSQSKPGTSVQTTSSGSGPFTDVRAAV 262
Scoring table: BLOSUM62 Gapop 10	BLOSUM62 Gapop 10.0 , Gapext 0.5
Searched:	283416 segs, 96216763 residues

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES	з ІД	L FINHU	L FNBO	2 S14428	2 A43908	2 I51279	2 A29355	2 A49173	AS		2 A56175		L A32230	2 T22674	2 T15099	L MMFFB1	2 T28811	2 S18188	2 A40043		•			2 T47158	2 S42612	2 T34022			T43	823868
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107	105	105	104.5	104.5	104	104	104	104	104	103.5	103.5	103.5	103.5	103	103
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## ALIGNMENTS

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A,Molecule type: protein
A,Molecule type: protein
A,Residues: 293-301 <GRI>
R,Galaycay, J.; Pande, H.; Lee, T.; Borsi, L.; Siri, A.; Shively, J.E.; Zardi, L.
J. Biol. Chem. 260, 12136-12141, 1985
J. Biol. Chem. 260, 12136-12141, 1985
A,Title: Primary structure of a DNA- and heparin-binding domain (domain III) in human pl
A,Reference number: A23901; MUID:86008277; PMID:3900070
A,Accession: A23901
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A,Residues: 616-677, Q', 679-703, 'PT', <CAL>
A;Residues: 616-677, Q', 679-703, 'PT', <CAL>
A;Residues: 616-677, Q', 679-703, 'PT', Sundelin, J.; Lind, P.; Peterson, P.A.
J. Biol. Chem. 257, 9593-9597, 1982
A,Title: The cell attachment domain of fibronectin. Determination of the primary structuly.
A,Reference number: A92386; MUID:82265604; PMID:7050098
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A;Residues: 1589-1630, T', 1722-2058 <GAR3>
A;Residues: 1589-1630, T', 1722-2058 <GAR3>
R;Tressel, T.; McCarthy, J.B.; Calaycay, J.; Lee, T.D.; Legesse, K.; Shively, J.B.; Panc B;ochem. J. 274, 731-738, 1991
A;Title: Human plasma fibronectin. Demonstration of structural differences between the A;Title: Human plasma fibronectin. Demonstration of structural differences between the A;Reference number: S14357; MUID:91190085; PMID:2012601
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A, Introns: 49/3; 1266/1; 1357/1; 1447/1; 1487/1; 1541/1; 1631/1; 1721/1; 1991/1; 2145/1
A, Introns: 49/3; 1266/1; 1357/1; 1447/1; 1487/1; 1541/1; 1631/1; 1721/1; 1991/1; 2145/1
A, Introns: 49/3; 1266/1; 1357/1; 1447/1; 1487/1; 1541/1; 1631/1; 1721/1; 1991/1; 2145/1
C, Superfamily: fibronectin; fibronectin type I repeat homology; fibronectin fibronectin fibronectin fibronectin fibronectin type I repeat homology (1F1)
F; 52-272/Domain: fibronectin type I repeat homology (1F2)
F; 71-11/20-25/Domain: fibronectin type I repeat homology (1F3)
F; 141-179/Domain: fibronectin fibr
R;Griffin, C.A.; Calaycay, J.; Shively, J.E.; Smith, R.L.
Thromb. Res. 43, 469-477, 1986
A;Title: Two plasma fibronectin fragments with different gelatin-binding properties.
A;Reference number: A60904; MUID:87019725; PMID:3532418
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A,Residues: 1441-1548 <PIE>
A,Note: residues 1524-1527 are responsible for the cell-binding activity
R,Garcia-Pardo, A.; Rostagno, A.; Frangione, B.
Biochem. J. 241, 923-228, 1987
A;Title: Primary structure of human plasma fibronectin. Characterization
A;Reference number: A32517; MUID:87241275; PMID:3393230
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F;308-342/Domain: fibronectin type I repeat homology <1F6>
F;306-401/Domain: fibronectin type II repeat homology <2F1>
F;420-461/Domain: fibronectin type II repeat homology <2F2>
F;470-508/Domain: fibronectin type II repeat homology <1F7>
F;518-555/Domain: fibronectin type I repeat homology <1F7>
F;516-599/Domain: fibronectin type I repeat homology <1F8>
F;60-692/Domain: fibronectin type II repeat homology <1F8>
F;60-692/Domain: fibronectin type III repeat homology <1F9>
F;60-692/Domain: homology <1F9>
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F;719-801/Domain: fibronectin type III repeat homology <3FB>
F;810-891/Domain: fibronectin type III repeat homology <3FC>
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A;Residues: 1614-1630, T', 1722-2081,2113-2244 <TKE>
R;Garcia-Pardo, A.; Pearlstein, E.; Frangione, B.
Biol. Chem. 260, 10325, 1985
A;Title: Primary structure of human plasma fibronectin.
A;Reference number: A23891; MUID:85261459; PMID:4019516
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A.Accession: A99529; MILD: 64272559; PMID: 6462919
A.Accession: A99529; MILD: 64272559; PMID: 6462919
A.Accession: A2011
A.Accession: A2014
A.Acce
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A, Molecule type: mRNA
A, Festidues: 2291-2386 < KO3-3
A, Cross-references: GB: KO0799; NID: g182681; PIDN: AAA52460.1; PID: g182684
B, Garcia-Pardo, A.; Pearlstein, E.; Frangione, B.
B, Garcia-Pardo, A.; Pearlstein, E.; Frangione, B.
A, Title: Primary structure of human plasma fibronectin.
A, Reference number: A92398; MUID: 84032463; PMID: 6630202
A, Accession: A92398
A, Molecule type: protein
A, Residues: 32-47, C', 49-51, S', 53-72, A', 74-290 < GAR1>
B, Garcia-Pardo, A.; Gold, L.1.
Arch. Biochem. Biophys: 304, 181-188, 1993
A, Title: Further characterization of the binding of fibronectin to gelatin reveals the A, Reference number: S34791; MUID: 93312001; PMID: 8323285
           Reference number: A91008; MUID:85284965; PMID:2992939
                                                                                                                              Status: nucleic acid sequence not shown
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A;Molecule type: protein
A;Residues: 291-300;551-560 <GAR2>
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Characterization of a 31,000-dal

Characterization of a 38 kDa dom

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Best Local Similarity 95.4 Matches 250; Conservative
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A/Accession: B21162
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C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 09-Jul-2004
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 09-Jul-2004
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 09-Jul-2004
R;Skorstengaard, K.; Jensen, M.S.; Sahl, P.; Petersen, T.E.; Magnusson, S.
Eur. J. Biochem. 161, 441-453, 1986
Eur. J. Biochem. 161, 441-453, 1986
A;Title: Complete primary structure of bovine plasma fibronectin.
A;Reference number: A26452; MUID:87054047; PMID:3780752
A;Molecule type: protein
A;Molecule type: protein
A;Molecule type: protein
A;Residues: 1-2265 <SKO
A;Ossa-references: UNIPROT:P07589
A;Molecule type: December: AR.; Vibe-Pedersen, K.; Baralle, F.E.
Proc. Natl. Acad. Sci. US.A. 80, 3218-3222, 1983
A;Title: Isolation and characterization of CONA clones for human and bovine fibronectine
A;Reference number: A21165; MUID:83221567; PMID:6304699
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             152 DIWRRPHETGGYMLECVCLGNGKGEWTCKPIAEKCFDHAAGTSYVVGETWEKPYQGWMMV
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                                                                                                                                                                                                                             Length 2386;
                            F;996-1077/Domain: fibronectin type III repeat homology <1FE>F;1086-1164/Domain: fibronectin type III repeat homology <3FE>F;1173-1258/Domain: fibronectin type III repeat homology <3FF>F;1266-1349/Domain: fibronectin type III repeat homology <3FF>F)
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    <3FD>
                                                                                                                                                                                                                         Query Match 100.0%; Score 1499; DB 1; Best Local Similarity 100.0%; Pred. No. 3.4e-109; Matches 262; Conservative 0; Mismatches 0;
F;906-988/Domain: fibronectin type III repeat homology
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C;Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 09-Jul-2004
C;Accession: S14428; S12455; Ā22319; S46203; S00459; A27252; I59049
R;Hynes, R.O.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241 RHTSLQTTSAGSGSFTDVRTAI 262
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F;718-800/Domain: fibronectin type III repeat homology <FN3B>
F;809-890/Domain: fibronectin type III repeat homology <FN3C>
F;905-987/Domain: fibronectin type III repeat homology <FN3E>
F;905-987/Domain: fibronectin type III repeat homology <FN3E>
F;1085-1164/Domain: fibronectin type III repeat homology <FN3E>
F;1085-1148/Domain: fibronectin type III repeat homology <FN3E>
F;1356-1439/Domain: fibronectin type III repeat homology <FN3I>
F;1356-1439/Domain: fibronectin type III repeat homology <FN3I>
F;1356-1439/Domain: fibronectin type III repeat homology <FN3I>
F;1537-1619/Domain: fibronectin type III repeat homology <FN3I>
F;1537-163/Domain: fibronectin type III repeat homology <FN3I>
F;1537-163/Domain: fibronectin type III repeat homology <FN3I>
F;1911-1933/Domain: fibronectin type III repeat homology <FN3I>
F;1911-133/Bejion: cell attachment (R-G-D) mocif
F;1932-273/Domain: fibronectin type III repeat homology <FN3I>
F;2191-233/Sylomain: fibronectin type III repeat homology <FN3I>
F;2191-233/Sylomain: fibronectin type III repeat homology <FN3I>
F;2191-233/Sylomain: fibronectin type II repeat homology <FN3I>
F;2193-2273/Domain: fibronectin type II repeat homology <FN3I>
F;238-2420/Domain: fibronectin type I repeat homology <FN3I>
F;238-2420/Domain: fibronectin type I repeat homology <FN3I>
F;238-2420/Domain: fibronectin type I repeat homology <FN3I>
F;238-240/Damain: fibronectin type I repeat homology <FN3I
F;248-101-2378/Damain: fibronectin type I repeat homology <FN3I
F;248-101-2378/Damain: fibronectin type I repeat homology <FN3I
F;248-101-2378/Damain: fibronectin type I repeat homology <FN3I
F;248-101-240/Damain: fibronectin type I repeat homology <FN3I
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C;Species: Xenopus laevis (African clawed frog)
C;Species: Xenopus laevis (African clawed frog)
C;Species: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 12-Feb-1999
C;Accession. 443908
R;DeSimone, D.W.; Norton, P.A.; Hynes, R.O.
Dev. Biol. 149, 357-369, 1992
A;Title: Identification and characterization of alternatively spliced fibronectin mRNAs A;Reference number: A43908; MUD:92111942; PMID:1730390
A;Accession: A43908
A;Accession: A43908
A;Accession: A43908
A;Accession: Compared with conceptual translation A;Molecule type: mRNA
A;Residues: 1-2481 cDES>
A;Cross-references: GB:M77820
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C;Superfamily: fibronectin; fibronectin type I repeat homology; fibronectin type II repeat homology; fibronectin type II repeat homology in the sequence of sequen
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RHV-LQSASAGSGSFTDVRTAI 293
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A.Rocession: S14428
A.Rocession: S14428
A.Recession: S14428
A.Rocession: A.S124
A.Rocession: A.S14
A.Rocession: A.Roc
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A;Cross-references: GB:MI1750; NID:g204164; PIDN:AAA41170.1; PID:g554437

C;Genetics:
A;Introns: 51/1; 94/1; 2416/3; 2454/3

C;Genetics:
A;Introns: 51/1; 94/1; 2416/3; 2454/3

C;Superfamily: fibronectin; fibronectin type I repeat homology; fibronectin type II repe
C;Keywords: alternative splicing; cell adhesion; collagen binding; disulfide bond; dupli
F;1-32,Domain: signal sequence #status predicted <NRT-
F;33-2477/Product: fibronectin type I repeat homology <IF1->
F;98-153-156/Domain: fibronectin type I repeat homology <IF2->
F;142-180/Domain: fibronectin type I repeat homology <IF5->
F;187-226/Domain: fibronectin type I repeat homology <IF5->
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F;308-342/Domain: fibronectin type II repeat homology <IF7->
F;410-461/Domain: fibronectin type II repeat homology <IF7->
F;410-461/Domain: fibronectin type II repeat homology <IF7->
F;410-569/Domain: fibronectin type II repeat homology <IF7->
F;618-555/Domain: fibronectin type II repeat homology <IF7->
F;619-692/Domain: fibronectin type II repeat homology <IF7->
F;609-692/Domain: fibronectin type III repeat homology <IF7->
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F;609-692/Domain: fibronectin type II repeat homology <IF7->
F;609-692/Domain: fibronectin type II repeat homology <IF7->
F;609-692/Domain: fibronectin type II
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A,Residues: 1586-1720, Tr,1722,1813-2477 <SC2>
R,Odermatt. E.; Tamkun, J.W.; Hynes, R.O.
Proc. Natl. Acad. Sci. U.S.A. 82, 6571-6575, 1985
A;Title: Repeating modular structure of the fibronectin gene: Relationship to protein st
A;Reference number: 159049; MUID:86016741; PMID:3863113
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A; Residues: 1-139;2382-2477 <PAT>
A; Cross-reteneces: EMBL:X05831
A; Note: the authors translated the codon CCT for residues 51 and 94 as Ala
R; Schwarzbauer, J.E.; Tamkun, J.W.; Lemischka, I.R.; Hynes, R.O.
A; A21-431, 1983
A; Title: Three different fibronectin mRNAs arise by alternative splicing within the codi
A; Reference number: A27252; MUID:84082067; PMID:6317187
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A;Residues: 1722-1810 «RES>
A;Cross-references: GB:M11750; NID:g204164; PIDN:AAA41170.1; PID:g554437
                                            submitted to the EMBL Data Library, July 1989
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                                                                                               Reference number: S14428
Accession: S14428
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fibronectin - chicken (fragment)
C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Species: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 09-Jul-2004
C;Accession, A.29355
R;Norton, P.A.; Hynes, R.O.
Myl. Cell. Biol. 7, 4297-4307, 1987
Myl. Cell. Biol. 7, 4297-4307, 1987
A;Fitler: Alternative splicing of chicken fibronectin in embryos and in normal and trans. A;Reference number: A29355; MuID:88142820; PMID:2830487
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matrix; glycoprotein; hete
     C;Superfamily: fibronectin, fibronectin type I repeat homology; fibronectin type : F;7-48/Domain: fibronectin type II repeat homology <2F2>
F;7-95/Domain: fibronectin type I repeat homology <1F>>
F;105-142/Domain: fibronectin type I repeat homology <1F8>
F;148-186/Domain: fibronectin type I repeat homology <1F8>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               173 PYQGWMWVDCTCLGEGSGRITCTSRNRCNDQDTRTSYRIGDTWSKKDNRGNLLQCICTGN 232
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                                                                                                                                                                                                                                                                                                                                     65 TCFDKYTGNTYRVGD-TYERPKDSMIWDCTCIG--AGRGRISCTIANRCHE-----GGQ
                                                                                                                                                                                                                                                                                                                                                                                                             116 SYKIGDTWRRPHETGGYMLECVCLGNGKGEWTC---KPIAEKCFDHAAGTSYVVGETWEK
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                                                                                                                                                                                Length 190;
                                                                                                                                                                                                                                         74; Indels
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                                                                                                                                                                                   Score 269; DB 2;
Pred. No. 4.3e-14;
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A;Cross-references: UNIPROT:P11722
C;Genetics:
                                                                                                                                                                                   Query Match
Best Local Similarity 33.5%;
Matches 63; Conservative 33
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Best Local Similarity
Matches 44; Conserv
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A;Accession: I51279
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molel type: mRNA
A;Residues: 1-190 <NAC>
A;Residues: 1-190 <NAC>
A;Cross-references: UNIPROT:Q91400; GB:S76886; NID:g914305; PIDN:AAB34250.1; PID:g914306
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C;Species: Notophthalmus viridescens, Triturus viridescens (eastern newt)
C;Species: Notophthalmus viridescens, Triturus viridescens (eastern newt)
C;Species: 13-59-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Accession: I51279
R;Nace, J.D.; Tassava, R.A.
Dev. byn. 202, I53-164, 1950-
A;Fitle: Examination of fibronectin distribution and its sources in the regr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              37 QOQÓVVÓPQG--TQDNHQKGCYDNGKYYQINQÓWERTYLGNTLVCTCYGGGRGFNCESKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DTWRRPHETGGYMLECVCLGNGKGEWTCKPIAEKCFDHAAGTSYVVGETWEKPYQGWMMV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DCTCLGEGNGRITCSSKNRCNDODIKTSYRIGDTWSKTDTRGNLLOCICTGNGRGEWKCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 QAQQMVQPQSPVAVSQSKPGCYDNGKHYQINQQWERTYLGNVLVCTCYGGSRGFNCESKP
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Cispedies: Gallus Gallus (chicken)
Cispedies: Gallus gallus (chicken)
Cipate: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
Cipate: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
Cipate: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
Cipate: 10-Sep-1999 #sequence_revision 10-Sep-1999; G33379; S01292; A30903
R;Jones, F.S.; Hoffman, S.; Cunningham, B.A.; Edelman, G.M.
Proc. Natl. Acad. Sci. U.S.A. 86, 1905-1909, 1989
A;Title: A detailed structural model of cytotactin: protein homologies, alternative RNA A;Reference number: A32230; WUID:89184536; PMID:2467292
A;Accession: A32230
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A;Residues: 1-1810 <JON>
A;Cross-references: UNIPROT:Q90824; GB:J04519; NID:g211717; PIDN:AAA48745.1; PID:g21171
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A,Status: preliminary
A,Gateure type: mRNA
A,Residues: 1-1044,1318-1810 <JO2>
A,Cross-references: GB:J04519
R,Spring, J: Beck, K; Chiquet-Ehrismann, R.
Cell 59, 325-334, 1989
A,Title: Two contrary functions of tenascin: dissection of the active sites by recombin
A,Reference number: A33379; MUID:90030407; PMID:2478295
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A; Accession: B33379
A; Astatus: preliminary; nucleic acid sequence not shown; not compared with conceptual transcension: C33379
A; Accession: C33379
A; Cross-references: GB:M23121
A; Molecule type: mRNA
A; Residues: 1-204,'G', 206-221,'A', 223-380,'D', 382-386,'H', 388-444,'HN', 447-450,'V', 452-87; Cross-references: GB:M23121
A; Cross-references: GB:M23121
B; B; Pearson, C.A.; Pearson, D; Shibahara, S.; Hofsteenge, J.; Chiquet-Ehrismann, R. BMBO J. 7, 2977-2982, 1988
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F;23-33/Domain: propeptide #status predicted <RRO>
F;34-1810/Product: tenascin 230K #status predicted <WAT>
F;223-249/Domain: EGF homology <EGFI>
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A;Residues: 27-181,'R',183-204,'G',206-221,'A',223-380,'D',382-386,'H',388-444,'HN',447
A;Cross-references: EMBL:X08030
                                                                                                                                                                                                                                                     122 TWRRPHETGGYMLECVCLGNGKGEWTCKPI---AEKCFDHAAGTSYVVGETWEKPYQGWM 178
                                                                                                                                                                                                                                                                                                                                                      441 --RCLHTYGWY--TCQCLDGWGGEICDRPMTCQTQQCFNG-----GTCLDKP---I 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  179 MYDCTCLGEGSGRITCTSRNRCNDQDTRTSYRIGDTWSKKDNRGNLLQCICTGNGRGEWK 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----KCVCKPGSSG-YN 530
                                  DKYTGNTYRVGDTYERPKDSMIWDCTCIGAGRGRISCTI-----ANRCHEGGQSYKIGD 121
                                                                                                                                        405 DRING------FSCDCSGTGYTGAFCQTNVDECDKNPCLINGG-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         485 GFQCLCPPEYTGEL-CQIAPSCAQQCPIDSECVGG----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     239 CERHTSVQTTSSGSG 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  531 CO-----TSTGDG 538
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adhesive plaque protein Mgfp2 precursor - Mediterranean mussel
C;Species: Mytilus galloprovincialis (Mediterranean mussel)
C;Date: 27-Apr.1955 #sequence_revision 03-Oct-1995 #text_change 09-Jul-2004
C;Accession: A56175
B;Inoue, K.; Takeuchi, Y.; Miki, D.; Odo, S.
J. Biol. Chem. 270. 6698-6701, 1995
A;Attle: Mussel adhesive plaque protein gene is a novel member of epidermal growth factce A;Recession: A56175, MUD:95204464; PMID:7896812
A;Accession: A56175
A;Access
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A; Status: preliminary
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-2139 cTEP>
A; Cross-references: UNIPROT: P10040; GB: M33753
A; Oto: the authors translated the codon GGC for residue 1928 as Cys, and TAT for residu
C; Genetics:
A; Gene: FlyBase: FlyBas
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R;Tepass, U.; Theres, C.; Knust, E.
Cell 61, 787-799, 1990
A;Title: crumbs encodes an EGF-like protein expressed on apical membranes of Drosophila A;Reference number: A35672; MUID:90263104; PMID:2344615
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97 AGRGRIS----CTIANRCHEGGQSYKIGDTWRRPHETGGYMLECVCLGNGKGE----WTC 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             111 GNFGRLCEKNVCS-PNPCKNNGKCSPLGKT-----GY--KCTCSGGYTGPRCEVHAC 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   353 QINP-CLNNGACVVIGG-----SGALTCECPKGYAGARCEVDTDECASQPCQNNGSCI 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KPIAEKCFDHAAGTSYVVGETWEKPYQGWMWVDCTCLGEGSGRITCTSR----NRCNDQD 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRISYRIGDIWSKKDNRGNLLQCICTGNGRGEWKCERHISVQT-----TSSGSGPP 255
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;Date: 21-Sep-1990 #sequence_revision 18-Nov-1992 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40 GNVLVCTCYGGSRGFNCESKPEAEETCFDKYTGNTYR----VGDTYERPKDSMIWDCTCIG
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8.6%; Score 128.5; DB 2; Length
Best Local Similarity 25.1%; Pred. No. 0.0096;
Matches 60; Conservative 21; Mismatches 85; Indels
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Best Local Similarity
Matches 59; Conserv
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206 TCSADKFGD-
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DD 1110 CNPSNPSACYQNAHCVYDAILNAHACKCVOGFKGDGTSCVPYAPATNCNLE 1160  QY 108 NR-CHEGGGSYKIGDTWRRPHETGGYMLECVCLGNGKGEWTCKPIABKCFDHAA 160  1161 PRICHANACVWHDTNAYBCICKPGSSGDGYTKCDVIETPRCTNCSIHA- 1210  QY 161 GTSYVVGETWEKPYQGWMVNDCTCLGGGSRTTCTSRNCNDQDTRTSYRIGDTWSKKDN 220  1211YCAQNPTSGAYQCKCNAGYNGHL-CVSMSSCLDDRSLCDE 1251  QY 221 RGNLLQCICTGNGRGEWKCERHTSVQTTSSGSPFTDVRA 260  1252 NADCVPGBAGHYVCNCHYGYHGDGRSCSPESSTRS 1286	RESULT 14 T1509 Hypothetical protein W03F8.5 - Caenorhabditis elegans C,Species: T15099 R,Johnson, D.; Bradshaw, H.; Keppler, D. Submitted to the EMBL Data Library, December 1997 A;Description: The sequence of C. elegans cosmid W03F8. A;Reference number: Z18293 A;Reference number: Z18293 A;Reference number: Z18293 A;Reference number: Z18293 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Status: preliminary; translated from GB/EMBL/DDBJ A;Residues: 1-1808 a,Odis A;Cross-references: UNIPROT:O44565; EMBL:AF039041; NID:g2736380; PID:g2736388; PIDN:AAB9 A;Cross-references: UNIPROT:O44565; EMBL:AF039041; NID:g2736380; PID:g2736380; PID:g	Query Match         7.7%; Score 115; DB 2; Length 1808;           Best Local Similarity 20.9%; Pred. No. 0.38;         102; Gaps 14;           Matches 62; Conservative 26; Mismatches 107; Indels 102; Gaps 14;           QY         8 PGSPVAVSQSKPGCY-DNGKHYQINQQMERTYLGNVLVCTCYGGSRGFNCESKPEAEET 65           Db         945 PGGPTSGTQHADTCYLRNSGNNTQ	RESULT 15 MWFFB1 laminin beta-1 chain precursor - fruit fly (Drosophila melanogaster) N;Alternate names: laminin chain B1 C;Species: Drosophila melanogaster C;Species: 30-Jun-1991 #sequence revision 30-Jun-1991 #text_change 09-Jul-2004 C;Accession: A28783; S14462; B28783 R;Montell, D.J.; Goodman, C.S. Cell 53, 463-473, 1988
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1013 ACLKCLYQTT 1022

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Search completed: September 30, 2005, 13:31:49 Job time : 42.4373 secs
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당
                                                                                                                     A; Molecule type: mRNA
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A; Crosd-uer: 1-1790 <MON1>
A; Crosd-uer: UNIPPOT: P11046; EMBL:M19525
R; Montell, D.J.; Goodman, C.S.
R; Molecule: Sequence of laminin B1 chain reve
A; Reference number: S14462
A; Accession: S14462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Description: interact with cells and with other basement membrane proteins to promote superfamily: laminin beta-1 chain; laminin-type EGF-like homology fixeywords: basement membrane; calcium binding; cell binding; coiled coil; extracellular 1.26/Domain: signal sequence #status predicted <SIG>
1.27-1790/Product: laminin beta-1 chain #status predicted <WAT>
1.288/Domain: VI <DOMS>
1.289-561/Domain: V <DOMS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F;51-56/Disulfide bonds: #status predicted
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F;1191,1194,1788/Disulfide bonds: interchain #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Gene: lamB1
A;Cross-references: FlyBase:FBgn0002527
A;Map position: 2L 28D
C;Complex: Laminins are trimers of an alpha-type, a beta-type, and a gamma-type laminin
    Title: Drosophila substrate adhesion molecule: sequence of laminin B1 chain reveals; Reference number: A28783; MUID:88210471; PMID:3365769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 959 NMLCHCQEGYSGSRCEICADNFFGNPDNGGTCSKCECSNNVDLYDTGN-----CDRQTG 1012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           802 VČESNGG----YCQCKPNVVGRQCDQCAPGTYGFG----PEGCKACDCNSIGSKDKYCD 852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --RGRISC----TIANRCHEGGQSYKIGDTWRRPHETGGYMLEC-VCLGNGKGEWTCKPIA 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                853 LITGOCOCVPNÍYGRECNOCOPGY-----WNFP-----ECRVCOCNGHAA-ICDPIO 898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  153 EKCFDHAAGTSYVVGETWEKPYQGWMWV------DCTC-----LGEGSGRITCTSRN 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       199 R--CNDQD----TRTSYRIGDTWSKKDNRGNLLQCIC-----TGNGRGEWKCERHTS 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                290-354/Domain: laminin-type EGF-like homology <LEO1>
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480-528/Domain: laminin-type EGF-like homology <LEO4>
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7.6%; Score 114; DB 1; Length 1790;
Best Local Similarity 24.4%; Pred. No. 0.45;
Matches 61; Conservative 18; Mismatches 97; Indels 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F;643-645/Region: cell attachment (R-G-D) motif
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85, Appl 1, Appli 1, Appli 10297, Ap 5, Appli 20, Appli 17, Appli 2, Appli 2, Appli 6, Appli 6, Appli 4, Appli

Sequence Sequence Sequence Sequence

US-09-949-016-5902 US-08-882-046-5 US-08-882-046-5 US-09-566-047-5 US-09-136-218-20 US-09-136-218-20 US-09-136-218-20

Sequence Sequence Sequence

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US-08-793-273C-4 PCT-US95-11684-4

ALIGNMENTS

US-09-121-457-2 US-08-882-046-6 US-08-899-232-2

US-09-566-047-6

Sequence 8 Sequence 6 Sequence 1 Sequence 5 Sequence 1

-09-566-047-2 -09-917-254-85

US-09-195-524-6

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CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/153,799
FILING DATE:
CLASSIFICATION A35
PRIOR APPLICATION TOWNER: US/08/153,799
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 07/847975
FILING DATE: 06-MAR-1992
PRIOR APPLICATION NUMBER: US 07/847975
FILING DATE: 29-APR-1999
PRIOR APPLICATION NUMBER: PS/APR-1990
PRIOR APPLICATION NUMBER: PS/APR-1990
PRIOR APPLICATION NUMBER: 26-APR-1990
PRIOR APPLICATION NUMBER: LS/APR-1990
PRIOR APPLICATION UNMBER: LS/APR-1991
ATTORNEY/AGRAFT TRFORMATION:
ANAME: CS/APR-1991
ATTORNEY/AGRAFT TRFORMATION:
ANAME: CS/APR-1991
ATTORNEY/AGRAFT TRFORMATION:
ANAME: CS/APR-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: R Hain Swope, BOC Health Care Inc
STREET: 100 Mountain Avenue
CITY: Murray Hill
STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 07974

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Swope, R Hain
REGISTRATION NUMBER: 24864
REFERENCE/DOCKET NUMBER: 92H832
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 665 2400
TELEFAX: (908) 771 6159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Ballance, David J
APPLICANT: Goodey, Andrew R
TITLE OF INVENTION: Polypeptides
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 16, Application US/08153799
Patent No. 5766883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 219484
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 2231 amino acids
TYPE: amino acid
1218
1218
1218
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1218
1219
1219
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48
2556
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TOPOLOGY:
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Sequence 16, Appli
Sequence 1, Appli
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Sequence 2, Appli
Sequence 1, Appli
Sequence 1, Appli
Patent No. 5455158
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580.396 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                     September 30, 2005, 08:57:15 ; Search time 33.6978 Seconds
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Sequence 1
Sequence 7
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Sequence 1
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Sequence 6
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Sequence 7
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                  GenCore version 5.1.6
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US-08-611-729A-10

US-08-611-729A-10

US-09-66-74-7

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US-09-56-740-7

US-09-56-140-7

US-09-59-56-18

US-09-19-85-1

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US-08-551-356-2
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US-08-283-857-1
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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181 DCTCLGEGSGRITCTSRNRCNDQDTRTSYRIGDTWSKKDNRGNLLQCICTGNGRGEWKCE 240
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                                                                                                                                                                                                                                              100.0%; Score 1499; DB 1; Length 2324; 100.0%; Pred. No. 2e-136; Cive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FIBRONECTIN FIBRIN-BINDING PEPTIDES, DNA CODING THEREFOR AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (BPO)
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APPLICATION NUMBER: US 08/283,857
FILING DATE: 01-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: BROWNY, ROGER L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: GOLD=1A PCTELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
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APPLICATION NUMBER: PCT/US95/09819
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TELEX: 248633
INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 2324 amino acids
               INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2324 amino acids
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Matches 262; Conservative
202-737-3528
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TITLE OF INVENTION: FIB
TITLE OF INVENTION: COD
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND
                                                                                              TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
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PCT-US95-09819-1
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APPLICANT: GOLD, Agueda A.
APPLICANT: BARON, Martin
APPLICANT: BARON, Martin
APPLICANT: CAMPBELL, Iain D.
APPLICANT: CAMPBELL, Iain D.
APPLICANT: WILLIAMS, Michael, J.
ITLE OF INVENTION: FIBRONECTIN FIBRIN-BINDING PEPTIDES, DNA
TITLE OF INVENTION: CODING THEREFOR AND USERS THEREOF
NUMBER OF SEQUENCES: 10
AUGHESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
                                                                                                                                                                                                                                                   Length 2231;
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MEDIUM TYPE: Floppy disk
COMPUTER: TEM PC compatible
COMPUTER: TEM PC compatible
COMPUTER: TEM PC compatible
CORRENT MINIOR SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/283,857
FILING DATE: 01-AUG-1994
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/714,134
APPLICATION DATA:
APPLICATION NUMBER: US 07/714,134
ATING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: BROWNY, ROGER L.
REGISTRATION NUMBER: 25,618
RESTRENCE/POCKET UNBER: GOLD=1A
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                              100.0%; Score 1499; DB 1;
100.0%; Pred. No. 1.9e-136;
ive 0; Mismatches 0;
                                                                                                                   NAME/KEY: Protein
LOCATION: 1..2231
OTHER INFORMATION: /note= "Human fibronectin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
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US-08-283-857-1
Sequence 1, Application US/08283857
Patent No. 5792742
; GENERAL INFORMATION:
                                                                    ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                      Best_Local Similarity 100.
Matches 262; Conservative
protein
NO
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STATE: D.C.
               HYPOTHETICAL: N
ORIGINAL SOURCE:
MOLECULE TYPE:
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DCTCLGEGSGRITCTSRNRCNDQDTRTSYRIGDTWSKKDNRGNLLQCICTGNGRGEWKCE 240
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                                                            Length 2386;
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CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/551,356

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION BATA:

APPLICATION NUMBER: US/08/349,762

FILING DATE:

APPLICATION NUMBER: US/07/998,271

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Holly, Julie A

REFERENCE/DOCKET NUMBER: 92-26

TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/08551356
Patent No. 5830700
GENERAL INFORMATION:
APPLICANT: Irani, Meher
TITLE OF INVENTION: HYBRID CROSS-LINKING PROTEINS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                            Query Match 100.0%; Score 1499; DB 2; Best Local Similarity 100.0%; Pred. No. 2e-136; Matches 262; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 1499;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFHONE: 206-547-8080 ext 322
TELEFAX: 206-548-2329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 98105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
, MOLECULE TYPE: protein US-09-016-366A-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
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                                                                                                 100.0%; Score 1499; DB 5; Length 2324; 100.0%; Pred. No. 2e-136; ive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Stevens, Richard L.
APPLICANT: Stevens, Chifu
TITLE OF INVENTION: INHIBITORS
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSER: Wolf, Greenfield & Sacks, P.C.
STREET: 600 Atlantic Avenue
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,366A
FILING DATE: January 30, 1998
CLASSIFICATION ADTA:
APPLICATION NUMBER: 60/037,090
FILING APPLICATION DATA:
APPLICATION NUMBER: 60/037,090
FILING DATE: 05-FEB-1997
ATTORNEY, AGENT INFORMATION:
NAMME: Plumer, Elizabeth R.
NAMME: Plumer, Elizabeth R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 36,637
REFERENCE/DOCKET NUMBER: B0801/7093
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
TELEFAX: 617-720-2441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RHTSVQTTSSGSGPFTDVRAAV 262
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 12
SEQUENCE CHARACTERISTICS:
LENGTH: 2386 amino acids
                                                                                                 Query Match 100.
Best Local Similarity 100.
Matches 262; Conservative
    single
                   TOPOLOGY: linear
MOLECULE TYPE: peptide
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STRANDEDNESS: sir
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  STRANDEDNESS:
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EAEETCFDKYTGNTYRVGDTYERPKDSMIWDCTCIGAGRGRISCTIANRCHEGGQSYKIG 120
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                   92 BAEETCFDKYTGNTYRVGDTYERPKDSMIWDCTCIGAGRGRISCTIANRCHEGGQSYKIG
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                                                                                                      152 DTWRRPHETGGYMLECVCLGNGKGEWTCKPIAEKCFDHAAGTSYVVGETWEKFYQGWMMV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: HAENDLER, BERNARD
APPLICANT: KRAETZSCHMAR, JOERN
APPLICANT: KRAETZSCHMAR, JOERN
APPLICANT: KRAETY
APPLICANT: WINTERHAGER, ELKE
APPLICANT: REGIDOR, PEDRO
APPLICANT: SCOTTI, SIMONE
TITLE OF INVENTION: METHOD FOR IN VITRO DIAGNOSIS OF ENDOMETRIOSIS
FILE REFERENCE: SCH-1789
CURRENT APPLICATION NUMBER: US/09/961,403
CURRENT PILING DATE: 2001-09-25
NUMBER OF SEQ ID NOS: 15
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Pred. No. 5e-136;
0; Mismatches 1; Indels 0
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5455158
-1
-2 PATENT NO. 5455158
-1
-2 APPLICANT: VOGEL, TIKVA; LEVANON, AVIGDOR; WERBER, MOSHE M.;
GUY, RACHEL, PANNET, AMOS
-1 TITLE OF INVENTION: FIBRIN BINDING DOMAIN POLYPEPTIDES AND
JUSES AND METHODS OF PRODUCING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 RHTSVQTTSSGSGPFTDVRAAV 262
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Patent No. 6780594
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Best Local Similarity 99.6%;
Matches 261; Conservative
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APPLICANT: HE-STUMPP, HOLGER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
LENGTH: 2386
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ORGANISM: Homo sapiens
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US-09-961-403-1
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                                                                                                                                                EAEETCFDKYTGNTYRVGDTYERPKDSM1WDCTC1GAGRGR1SCT1ANRCHEGGQSYK1G
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                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Irani, Meher H.
TITLE OF INVENTION: HYBRID CROSS-LINKING PROTEINS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: ZymoGenetics, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/12687
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION
APPLICATION NUMBER: US 07/998,271
FILING DATE: 31-DEC-1992
ATTORNEY/AGENT INFORMATION:
  100.0%; Pred. No. 2.1e-136; ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Parker, Gary E
REGISTRATION NUMBER: 31-648
REFRENCE/POCKET NUMBER: 92-26PC
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1806-547-8080 ext 322
                                                                                                                                                                                                                                                                                                                                                                                                     RHTSVQTTSSGSGPFTDVRAAV 262
                                                                                                                                                                                                                                                                                                                                                                                                                             E: ZymoGenetics, Inc.
4225 Roosevelt Way, N.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application PC/TUS9312687
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 2446 amino acid
                     262; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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  Similarity
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Matches 26
  Best Local
Matches 26
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181 DCTCLGEGSGRITCTSRNRCNDQDTRTSYRIGDTWSKKDNRGNLLQCICTGNGRGEWKCE 240
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                                                        DTWRRPHETGGYMLECVCLGNGKGEWTCKPIAEKCFDHAAGTPYVVGETWEKPYQGWMYV 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       269 ISINYRTEIDKPSQNEGLNQPTDDSCFDPYTVSHYAVGDEWERMSESGFKLL--CQCLGF 326
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                               DTWRRPHETGGYMLECVCLGNGKGEWTCKPIAEKCFDHAAGTSYVVGETWEKPYQGWMVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 QQMVQP--QSPVAVSQSKPGCYDNGKHYQINQQWERTYLGNVLVCTCYGGSRGFNCESKP
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                                                                                                                                                                                                                                                                                                                                            Sequence 9, Application US/08836854
Patent No. 5824547
GENERAL INFORMATION:
APPLICANT: HASHINO, Kimikazu
APPLICANT: MATSUSHITA, Hideyuki
APPLICANT: MATO, Ikunoshin
TITLE OF INVENTION: METHOD OF PRODUCTION OF TRANSFECTED CELLS
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 474;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19.7%; Score 295.5; DB 2; 33.8%; Pred. No. 2.1e-20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: Browdy and Neimark
STREET: 419 Seventh Street N.W. Ste. 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 29-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 317721/1994
FILING DATE: 29-NOV-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 227 ÓEFTVÞGSKSTATISGLKÞGV-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/836,854
                                                                                                                                                                                                    241 RHTSVQTTSSGSGPFTDVRAAV 262
                                                                                                                                                                                                                           RHTSVQTTSSGSGPFTDVRAAV 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Browdy, Roger L. REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: HATELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (202) 628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (202) 737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  474 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 33.89
Matches 72; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (202) 737-352
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                   US-08-836-854-9
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                                                                      124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DIWRRPHETGGYMLECVCLGNGKGEWTCKPIAEKCFDHAAGTSYVVGETWEKPYQGWMMV 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DCTCLGEGSGRITCTSRNRCNDQDTRTSYRIGDTWSKKDNRGNLLQCICTGNGRGEWKCE 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EAEETCFDKYTGNTYRVGDTYERPKDSMIWDCTCIGAGRGRISCTIANRCHEGGQSYKIG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    124 DTWRRPHETGGYMLECVCLGNGKGEWTCKPIAEKCFDHAAGTPYVVGETWEKPYQGWMWV 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DCTCLGEGSGRITCTSRNRCNDQDTRTSYRIGDTWSKKDNRGNLLQCICTGNGRGEWKCE 243
                                                                                                                                                                                                                                                                                                                                                                                                                    1 QAQQMVQPQSPVAVSQSKPGCYDNGKHYQINQQWERTYLGNVLVCTCYGGSRGFNCESKP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 QAQQMVQPQSPVAVSQSKPGCYDNGKHYQINQQWERTYLGNVLVCTCYGGSRGFNCESKP 63
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APPLICANT: VOCEL, TIKVA; LEVANON, AVIGDOR; WERBER, MOSHE M.;
GUY, ACCHEL, PAMCEL, AMOS
TITLE OF INVENTION: FIBRIN BINDING DOMAIN POLYBEPTIDES AND
TITLE OF INVENTION: FIBRIN BINDING DOMAIN POLYBEPTIDES AND
WUMBER OF SEQUENCES: 20
CURRENT APPLICATION DATA:
PILLING DATE: 04-MAY-1993
PRIOR APPLICATION NUMBER: 526,397
FILLING DATE: 21-MAY-1990
PILLING DATE: 21-MAY-1990
PILLING DATE: 21-MAY-1990
PILLING DATE: 28-APR-1999
                                                                                                                                                                                                                                                                                                                              Score 1494; DB 6; Length 2327;
Pred. No. 6e-136;
0; Mismatches 1; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99.7%; Score 1494; DB 6; Length 2327; 99.6%; Pred. No. 6e-136; ive 0; Mismatches 1; Indels 0
NUMBER OF SEQUENCES: 20
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/58,241
FILING DATE: 04-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 26,397
FILING DATE: 21-MAY-1990
APPLICATION NUMBER: 345,952
FILING DATE: 28-APR-1999
APPLICATION NUMBER: 29-1951
FILING DATE: 29-DEC-1988
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FILING DATE: 29-DEC-1988
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Best Local Similarity 99.6
Matches 261; Conservative
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Matches 261; Conservative
                                                                                                                                                                                                                                                                 LENGTH: 2327
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                                                                                                                                                                                                                                          SEQ ID NO:1
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;Patent No.
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CITY: New York
STATE: New York
COUNTR: U.S.A.
ZOUNTR: U.S.A.
ZOB: 10036-2787
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: STEM: PC-DOS/MS-DOS
SOFTWARE: PAtentIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/142,449B
                        382 DD--GKTYHVGEQWQKEYLG-AICSCTCFGGQRG 412
157 DHAAGTSYVVGETWEKPYQGWMMVDCTCLGEGSG 190
                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Nels T. Lippert, White & Case STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Lippert, Nels T.
REGISTRATION NUMBER: 25,888
REFERENCE/DOCKET NUMBER: 1145358-304
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)-819-8582
TELEPHONE: (212)-819-8582
INFORMATION FOR SEQ ID NO: 14: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 омЫЕК: US/08/142,449В
24-NOV-1994
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US-08-400-159-10
US-08-400-159-10
Sequence 10, Application US/084Q0159
Patent No. 5869282
GENERAL INFORMATION:
APPLICANT: Henrique, Domingos M.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : 188 amino acids
amino acid
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MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            223 QEFTVPGSKSTATISGLKPGV-------DYTITVYAVTGRGDS---PASSKP 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97 AGRGRISCTIANRCHEGGQSYKIGDTWRRPHETGGYMLECVCLGNGKGEWTCKPIAEKCF 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GRGRISCTIANRCHEGGQSYKIGDTWRRPHETGGYMLECVCLGNGKGEWTCKPIAEKCFD 157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50;
                                                                                                                                                                                                                                                                                          APPLICANT: HASHINO, Kimikazu
APPLICANT: MATSUSHITA, Hideyuki
APPLICANT: KATO, Ikunoshin
APPLICANT: KATO, Ikunoshin
MITLE OF INVENTION: 21
CORRESPONDENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19.7%; Score 295; DB 2; Length 422; 33.6%; Pred. No. 2e-20; tive 22; Mismatches 70; Indels !
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                         386 D--GKTYHVGEQWQKEYLG-AICSCTCFGGQRG 415
                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street N.W. Ste. 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DCT/JP95/02425
FILING DATE: 29-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 317721/1994
FILING DATE: 29-NOV-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Browdy, Roger L. REGISTRATION NUMBER: 25,618
REGISTRATION NUMBER: HASHINO=1
TELECOMMUNICATION:
TELEPHONE: (202) 628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/836,854
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                          Sequence 12, Application US/08836854 Patent No. 5824547 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 422 amino acids
TYPE: amino acid
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Best Local Similarity 33.6<sup>3</sup>
Matches 72; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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US-08-836-854-12
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120 GDTWRRPHETGGYMLECVCLGNGKGEWTCKPIAEKCFDHAAGTSYVVGETWEKPYQGWMM 179
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US-08-142-449B-14

Sequence 14, Application US/08142449B

Sequence 14, Application US/08142449B

Patent No. 5668104

GENERAL INFORMATION:

APPLICANT: Nakahata, Tatsutoshi
APPLICANT: Sudo, Tetsuo

APPLICANT: Sudo, Tetsuo

TITLE OF INVENTION: Physiologically Active Protein and
TITLE OF INVENTION: Hematopoietic Stem Cell Growth Agent
NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 19.6%; Score 294.5; DB 1; Length 188; Best Local Similarity 43.5%; Pred. No. 8e-21; Matches 57; Conservative 19; Mismatches 46; Indels 9
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58 SKPEA--EETCFDKYTGNTYRVGDTYERPKDSMIWDCTCIGAGRGRISCTIA-----N 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             678 SRDSQCDEATC--NNGGTCYDEGDTFK-----CMC-PAGWEGATCNIARNSSCLPN 725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    109 RCHEGGQSYKIGDTWRRPHETGGYMLECVCLGNGKGEWTCKPIAEKCFDHA---AGTSYV 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          726 PCHNGGTCVVSGDSF-----TCVCKEGWEGP-TCTQNTNDCSPHPCYNSGTC-V 772
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94;
                                                                                                 NUCLECTIDE AND PROTEIN SEQUENCES OF THE SERRATE GENE AND METHODS BASED THEREON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1193;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         830 QEVTGRPCFTSIRVMPDGAKWDDDCNTCQCL---NGK 863
                                                                                                                                                                                                                                                                                                                                     COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/611,729A
FILING DATE: 06-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                201 NDQDTR---TSYRIGDTWSKKDNRGNLLQCICTGNGR 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
10.6%; Score 159; DB 3;
Best Local Similarity 26.4%; Pred. No. 1.2e-06;
Matches 73; Conservative 22; Mismatches 88
                      Fleming, Robert J.
Artavanis-Tsakonas, Spyridon
                                                                                                                                                                                ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   166 VGETWEKPYQ-----GWMMVDC----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : .....crdONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66.41 PENNIE
; INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
TWOP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ish-Horowicz, David
Henrique, Domingos M.P.
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Sequence 10, Application US/09195524

Patent No. 6703489

GENERAL INFORMATION:
APPLICANT: Henrique, Domingos M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/ACENT INPORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18, 872
REFERENCE/DOCKET NUMBER: 73
TELECOMMUNICATION INFORMATION:
                                                                Mann, Robert S
Gray, Grace E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , MOLECULE TYPE: protein US-08-611-729A-10
                                                                                                                                        NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie &
                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                       APPLICANT: Artavanis
APPLICANT: Mann, Robs
APPLICANT: Gray, Grad
TITLE OF INVENTION: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               unknown
                                                                                                                                                                                                                                        3: New York
RY: U.S.A.
10036-2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RCHEGGQSYKIGDIWRRPHETGGYMLECVCLGNGKGEWTCKPIAEKCFDHA---AGTSYV 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        726 PCHNGGTCVVSGDSF-----TCVCKEGWEGP-TCTQNTNDCSPHPCYNSGTC-V 772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----- LGNVLVCTCYGGSRGFNCE 57
      Length 1193;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 88; Indels
                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 07-MAR-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   830 QEVIGRPCFISIRVMPDGAKWDDDCNTCQCL---NGK 863
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10.6%; Score 159; DB 2; 26.4%; Pred. No. 1.2e-06; tive 22; Mismatches 88;
Myat, Anna M.
Fleming, Robert J.
Artavanis-Tsakonas, Spyridon
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Henrique, Domingos M.P.
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US-08-611-729A-10
US-08-611-729A-10
Sequence 10, Application US/08611729A
Patent No. 6004924
GENERAL INFORMATION:
APPLICANT: Henrique, Dowingos M.P
APPLICANT: Henrique, Domingos M.P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFRENCE/DOCKET NUMBER: 7326
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (212) 869-974/8864
TELEX: 66141 PENNIE
INFORMATION FOR END ID: SEQUENCE CHARACTERISTICS:
LENGTH: 1193 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 26.4%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , MOLECULE TYPE: protein US-08-400-159-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid
                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 10036-2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
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109 RCHEGGQSYKIGDTWRRPHETGGYMLECVCLGNGKGEWTCKPIAEKCFDHA---AGTSYV 165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94; Gaps
                   APPLICANT: Myat, Anna M.
APPLICANT: Fleming, Robert J.
APPLICANT: Aravanis-Tsakonas, Spyridon
APPLICANT: Mann, Robert S.
APPLICANT: Mann, Robert S.
APPLICANT: Gray, Grace E.
TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF THE TITLE OF INVENTION: SERRATE GENE AND METHODS BASED THEREON CORRESPONDENCES 20
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10.6%; Score 159; DB 4; Length 1193; 26.4%; Pred. No. 1.2e-06; tive 22; Mismatches 88; Indels 94
                                                                                                                                                                                                                                                                    CITY: New York
STATE: New York
COUNTR: U.S.A.
ZIP: 10036-271.
ZIP: TOUGE-271.
ZOMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/195,524
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                201 NDQDTR---TSYRIGDTWSKKDNRGNLLQCICTGNGR 234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21 CYDNGKHYQ--INQQWERTY-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 06-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7326-037
TELECOMMUNICATION INFORMATION:
TELEPRONE: (212) 790-9090
TELERX: (6141 PENNIE
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARATREEFICE:
                                                                                                                                                                                                                              ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
Lewis, Julian H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1193 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 26.49
Matches 73; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-195-524-10
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GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

September 30, 2005, 08:57:20; Search time 197.974 Seconds (without alignments) 549.366 Million cell updates/sec Run on:

1 QAQQMVQPQSPVAVSQSKPG......TSVQTTSSGSGPFTDVRAAV 262 US-09-492-971B-15\_COPY\_4\_265 Perfect score: Sequence:

Title:

**BLOSUM62** Scoring table:

1846076 seqs, 415116000 residues Gapop 10.0 , Gapext 0.5 Searched:

Total number of hits satisfying chosen parameters: Minimum DB seq length: 0 Maximum DB seq length: 2000000000

1846076

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Published Applications AA:\*

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19: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep:\*
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22: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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	_	64,	70,	98,	98	677,	677,	677,	52,	52,	354,	1066
	Description	Sequence	Seguence	Sequence	Sequence	Sequence		Sequence	Sequence	Sequence	Sequence	Sequence
	QΙ	US-10-171-311-64	US-10-236-031B-70	US-10-374-979-98	US-10-182-936A-98	US-10-477-238A-677	US-10-680-287A-677	US-10-477-173-677	US-10-144-194A-52	US-10-491-566-52	US-10-741-601-354	US-10-741-600-1066
		14	15	15	15	16	16	11	15	16	16	11
	Watch Length DB	2328	2328	2328	2328	2328	2328	2328	463	463	642	642
ا ع ع	Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	99.7	7.66	99.7	99.7
	Score	1499	1499	1499	1499	1499	1499	1499	1495	1495	1495	1495
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359, A 1072, 356, A 1069, 4, App	Sequence 1075, Ap Sequence 104, App Sequence 235, App Sequence 3, Appli Sequence 94, Appli Sequence 94, Appli	0 1 1 1 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	equence 1137, equence 28, A equence 17, Ag equence 206, equence 32, A equence 1071,	Sequence 59, Appl Sequence 9, Appli Sequence 9, Appli Sequence 4, Appli Sequence 2, Appli Sequence 8, Appli Sequence 52638, A
-10-741-601-359 -10-741-600-107 -10-741-601-356 -10-741-600-106 -10-236-392-4 -10-741-601-363	1 1 2 8 6 7	10-741-601-36 10-491-566-10 10-741-600-10 10-741-600-10 10-852-335A-1	-10-28/436A-11 -11-040-130-28 -10-741-601-360 -10-788-792-206 -10-618-281-32 -10-741-600-107	US-10-868-577A-59 US-10-465-758-4 US-10-485-758-4 US-10-235-49 US-10-235-4 US-10-279-733-8 US-10-450-763-52638 US-10-450-763-52634 US-10-450-763-52634
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## ALIGNMENTS

APPLICANT: Chen, Yan
APPLICANT: Chen, Yan
APPLICANT: Chen, Yan
APPLICANT: Chen, Yan
APPLICANT: Amathar, John
APPLICANT: Monahan, John
APPLICANT: Manahar, John
APPLICANT: Manahar, John
APPLICANT: Manahar, John
APPLICANT: Manahar, John
APPLICANT: Glatt, Karen
APPLICANT: Glatt, Manjula
APPLICANT: OF CERVICAL CANCER
TITLE OF INVENTION: DOF CERVICAL CANCER
TITLE OF INVENTION: OF CERVICAL CANCER
TITLE OF INVENTION: OF CERVICAL CANCER
FILE REFERENCE: MAL-035
CURRENT FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 60/298,159
TYPE: PRIOR APPLICATION NUMBER: US 60/298,159 Sequence 64, Application US/10171311; Publication No. US20030087270A1; GENERAL INFORMATION: APPLICANT: Schlegel, Robert , ORGANISM: Homo sapiens US-10-171-311-64

Query Match

100.0%; Score 1499; DB 14; Length 2328;

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LENGTH: 2328
             RESULT 3
US-10-374-979-98
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; Pred. No. 7.9e-130; 0; Mismatches 0;
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 100.0%;
                Matches 262; Conservative
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US-10-236-031B-70
    Best Local Similarity
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APPLICANT: Anisowicz, Anthony
APPLICANT: Anisowicz, Anthony
APPLICANT: Bhat. Bheem
APPLICANT: Bhat. Bheem
APPLICANT: Banganez, Veronique
APPLICANT: Banganez, Veronique
APPLICANT: Taworsky, Paul
APPLICANT: Yaworsky, Paul
APPLICANT: Yaworsky, Paul
TITLE OF INVENTION: Reagents and Method for Modulating DKK-Mediated Interactions
FILE REPERENCE: 032796-143
CURRENT APPLICATION NUMBER: DCT/US02/15982
PRIOR APPLICATION NUMBER: US 60/291,311
PRIOR PILING DATE: 2001-05-17
PRIOR PILING DATE: 2001-05-17
PRIOR FILING DATE: US 60/291,311
PRIOR FILING DATE: US 60/391,311
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                                                                           THE REFERENCE: 032796-021

TITLE OF INVENTION: THE HIGH BONE MASS GENE OF 11q13.3

FILE REFERENCE: 032796-021

CURRENT APPLICATION NUMBER: US/10/374.979

CURRENT FILING DATE: 2003-03-04

PRIOR FILING DATE: 2000-04-05

PRIOR FILING DATE: 2000-04-05

PRIOR FILING DATE: 2000-04-05

PRIOR FILING DATE: 2000-04-05

PRIOR FILING DATE: 1999-01-13

PRIOR FILING DATE: 1999-01-13

PRIOR FILING DATE: 1999-01-13

PRIOR FILING DATE: 1999-01-13

PRIOR FILING DATE: 1998-01-13

PRIOR FILING DATE: 1998-01-13

PRIOR FILING DATE: 1998-10-23

NUMBER OF SEQ ID NOS: 109
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Sequence 98, Application US/10374979
Publication No. US20030219793A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Homo sapiens
US-10-374-979-98
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US-10-182-936A-98
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TYPE: PRT
ORGANISM: Homo sapiens
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Publication No. US20040221326A1

FEBRERAL INFORMATION:
APPLICANT: Babij, Philip
APPLICANT: Babij, Philip
APPLICANT: Babij, Philip
APPLICANT: Bodine, Peter Van Nest
TITLE OF INVENTION: Transgenc Animal Model of Bone Mass Modulation
FILE REFERENCE: 1032796-212
CURRENT APPLICATION NUMBER: US/10/477,238A
CURRENT APPLICATION NUMBER: US 60/290,071

FRIOR APPLICATION NUMBER: US 60/291,311
PRIOR APPLICATION NUMBER: US 60/291,311
PRIOR PELING DATE: 2001-05-17
FRIOR PAPLICATION NUMBER: US 60/353,058
FRIOR FILING DATE: 2002-02-01
FRIOR FILING DATE: 2002-02-01
FRIOR FILING DATE: 2002-03-04
FRIOR FILING DATE: 2002-03-04
FRIOR FILING DATE: 2002-03-04
FRIOR APPLICATION NUMBER: US 60/361,293
FRIOR PLING DATE: 2002-03-04
FRIOR APPLICATION NUMBER: US 60/361,293
FRIOR PLING DATE: 2002-03-04
FRIOR APPLICATION NUMBER: US 60/361,293
FRIOR APPLICATION NUMBER: US 60/361,293
FRIOR APPLICATION NUMBER: US 60/361,293
FRIOR APPLICATION NUMBER: DOS 60/361,293
FRIOR APPLICATION NUMBER: PAGENCE OF 60/361,293
FRIOR APPLICATION NUMBER: DOS 60/361,293
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100.0%; Pred. No. 7.9e-130;
ive 0; Mismatches 0;
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100.0%; Pred. No. 7.9e-130;
Live 0; Mismatches 0;
PRIOR FILING DATE: 2002-02-01
PRIOR APPLICATION NUMBER: US 60/361,293
PRIOR FILING DATE: 2002-03-04
NUMBER OF SEQ ID NOS: 216
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 98
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                                                                                                                                      TYPE: PRT
ORGANISM: Homo sapiens
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US-10-182-936A-98
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                                                                                                                      LENGTH: 2328
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; Sequence 677, Application US/10680287A
; Publication No. US20040244069A1
; GRNERAL INFORMATION:
    APPLICANT: Babij, Philip
; APPLICANT: Babij, Philip
; APPLICANT: Back, Frederick J. III
APPLICANT: Back, Frederick J. III
APPLICANT: Bodine, Peter Van Nest;
TITLE OF INVENTION: Transgenic Animal Model of Bone Mass Modulation
; FILE REFERENCE: 203796-179
; CURRENT FILING DATE: 2003-10-08
; PRIOR FILING DATE: 2003-0-08
; PRIOR PAPLICATION NUMBER: CT/US02/14876
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: US 60/290,071
; PRIOR FILING DATE: 2001-05-17
; PRIOR FILING DATE: 2002-02-01
; PRIOR FILING DATE: 2002-02-01
; PRIOR FILING DATE: 2002-02-01
; PRIOR FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 812
; SOFTWARE: FastSEQ for Windows Version 4.0
                                     65 BABETCFDKYTGNTYRVGDTYERPKDSMIWDCTC1GAGRGRISCTIANRCHEGGQSYKIG
EAEBTCFDKYTGNTYRVGDTYERPKDSMIWDCTCIGAGRGRISCTIANRCHEGGQSYKIG
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Matches 262; Conservative
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US-10-144-194A-52
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US-10-144-194A-52

Sequence 52, Application US/10144194A

Publication No. US20030215809A1

GENERAL INFORMATION:
APPLICANT: OriGene Technologies Inc
TITLE OF INVENTION: Regulated Breast Cancer Genes
FILE REFERENCE: 3U 103 R1

CURRENT APPLICATION NUMBER: US/10/144,194A

CURRENT FILING DATE: 2002-06-12

WUMBER OF SEQ ID NOS: 114

SOFTWARE: PatentIn version 3.0

SEQ ID NO 52
                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 1086
SOFTWARE: FastSEQ for Windows Version 4.0
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US-10-477-173-677
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ORGANISM: Homo sapiens
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Score 1495; DB 15;
Pred. No. 3e-130;
0; Mismatches 1;
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Publication No. US20040249144A1
GENERAL INFORMATION:
TITLE OF INVENTION:
FILE REPERENCE: 30 103 R1
CURRENT APPLICATION NUMBER: US/10/491,566
CURRENT FILING DATE: 2004-04-05
NUMBER OF SEQ ID NOS: 148
SOFTWARE: Patentin version 3.1
SEQ ID NO 52
LENGTH: 463
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US-10-741-601-354
; Sequence 354, Application US/10741601
99.7%;
                           Best Local Similaria,
Matches 261; Conservative
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US-10-491-566-52
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US-10-741-600-1072

Sequence 1072, Application US/10741600

Sequence 1072, Application US/10741600

Publication No. US20050026169A1

GENERAL INFORMATION:

APPLICANT: CARGILL, Michele et al.

TITLE OF INVENTION: MCCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF;
FILE REPERENCE: CL001499

CURRENT APPLICATION NUMBER: US/10/741,600

CURRENT FILING DATE: 2003-12-22

NUMBER OF SEQ ID NOS: 73997

SOFTWARE: PastSEQ for Windows Version 4.0

SEQ ID NO 1072
                                                                           EAEETCFDKYTGNTYRVGDTYBRPKDSMIWDCTC1GAGRGRISCT1ANRCHEGGGSYKIG 151
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                                                                                                                                                                                                                                                                                                                        Sequence 359, Application US/10741601
Publication No. US20040166519A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
FILE REPERENCE: CLO01500
CURRENT PELING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 26415
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 359
LENGTH: 657
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Pred. No. 4.5e-130;
0; Mismatches 1;
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Best Local Similarity 99.6%;
Matches 261; Conservative
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US-10-741-601-359
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ORGANISM: Homo sapiens
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Publication No. US20050026169A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
FILE REPERENCE: CL001499
CURRENT APPLICATION NUMBER: US/10/741,600
CURRENT FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 73997
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1066
LENGTH: 642
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Publication No. US20040166519A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENERIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001500
CURRENT APPLICATION NUMBER: US/10/741,601
CURRENT FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 26415
SOFTWARE: PASISEQ for Windows Version 4.0
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99.7%; Score 1495; DB 17; Length 642;
Best Local Similarity 99.6%; Pred. No. 4.4e-130;
Matches 261; Conservative 0; Mismatches 1; Indels 0
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; ORGANISM: Homo sapiens
US-10-741-601-354
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; ORGANISM: Homo sapiens
US-10-741-600-1066
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TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001500
CURRENT APPLICATION NUMBER: US/10/741,601
CURRENT FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 26415
SOFTWARE: FASESEQ for Windows Version 4.0
SEQ ID NO 356
LENGTH: 984
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Pred. No. 7.1e-130;
0; Mismatches 1; Indels 0
                            99.7%; Score 1495; DB 17; Length 657; 99.6%; Pred. No. 4.5e-130; ive 0; Mismatches 1; Indels 0
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                                             Best Local Similarity 99.6
Matches 261; Conservative
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US-10-741-601-356
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261; Conserv
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US-10-741-600-1069
JS-10-741-600-1072
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Best Local S:
Matches 261
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Sequence 1069, Application US/10741600
Publication No. US20050026169A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF FILE REPERENCE: CL001499
CURRENT APPLICATION NUMBER: US/10/741,600
CURRENT FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 73997
SSOFTWARE: FastSEQ for Windows Version 4.0
SSOFTWARE: PastSEQ for Windows Version 4.0
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Pred. No. 7.1e-130;
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Best Local Similarity 99.6%;
Matches 261; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Homo sapiens
US-10-741-600-1069
```